

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2005, 22:56:08 ; Search time 164.45 Seconds
(without alignment)

45.484 Million cell updates/sec

Title: US-09-932-322-1

Perfect score: 44

Sequence: 1 XXXCXPTGCGXX 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02: *
1: uniprot_gprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	36	81.8	192 2 Q98AR9	Q98AR9 rhizobium 1
2	36	81.8	360 2 Q86AK7	Q86AK7 dicystostei
3	36	81.8	546 2 Q8KJ72	Q8KJ72 rhizobium 1
4	36	81.8	601 2 Q7M4J3	Q7M4J3 dicystostei
5	35	79.5	148 2 Q9N018	Q9N018 macaca faec
6	35	79.5	148 2 Q95KD2	Q95KD2 macaca faec
7	35	79.5	571 2 Q9AQP5	Q9AQP5 pseudomonas
8	34	77.3	113 2 Q726J7	Q726J7 homo sapien
9	34	77.3	145 1 PA2X_NOTSC	P20146 notochis sc
10	34	77.3	167 2 Q7UVV9	Q7UVV9 synecococ
11	34	77.3	312 2 Q98UV3	Q98UV3 arabidopsis
12	34	77.3	465 2 Q6TVH9	Q6TVH9 bovine papu
13	34	77.3	465 2 AAR98366	AAR98366 bovine pa
14	34	77.3	574 2 Q8LJ36	Q8LJ36 oryza sativ
15	34	77.3	598 2 Q86AK4	Q86AK4 dicystostei
16	34	77.3	2217 2 Q6T825	Q6T825 laaba vitus
17	34	77.3	2217 2 AAO59515	AAO59515 laaba vit
18	33	75.0	464 2 Q7XV21	Q7XV21 oryza sativ
19	33	75.0	1058 2 Q9LEZ5	Q9LEZ5 arabidopsis
20	33	75.0	1468 2 Q80TF6	Q80TF6 mus musculi
21	32	72.7	64 2 Q92U25	Q92U25 rhizobium m
22	32	72.7	123 2 Q92EM4	Q92EM4 listeria in
23	32	72.7	520 2 Q628K1	Q628K1 oryza sativ
24	32	72.7	520 2 BAD15642	BAD15642 oryza sat
25	32	72.7	1152 2 Q9P126	Q9P126 arabidopsis
26	31	70.5	162 2 Q9WU17	Q9WU17 mesocricetu
27	31	70.5	166 2 Q8TA15	Q8TA15 dirosophila
28	31	70.5	239 2 Q93KV9	Q93KV9 streptomyce
29	31	70.5	342 2 Q6VMA4	Q6VMA4 streptomyce
30	31	70.5	342 2 AAR30165	AAR30165 streptomy
31	31	70.5	361 2 Q8ECT9	Q8ECT9 shewanella

32	31	70.5	482 2 Q9LZ88	Q9LZ88 arabidopsis
33	31	70.5	615 2 Q22886	Q22886 caenorhabdi
34	30	68.2	66 2 Q7N375	Q7N375 photorhabdu
35	30	68.2	78 2 P90569	P90569 plasmidium
36	30	68.2	95 2 P77130	P77130 escherichia
37	30	68.2	100 1 CHA3 BOMMO	P08929 bombyx mori
38	30	68.2	114 2 Q8M078	Q8M078 caenorhabdi
39	30	68.2	119 2 Q8P958	Q8P958 xanthomonas
40	30	68.2	129 1 CHA1 BOMMO	P08626 bombyx mori
41	30	68.2	132 1 CHA2 BOMMO	P08625 bombyx mori
42	30	68.2	133 2 Q9LIW4	Q9LIW4 oryza sativ
43	30	68.2	150 2 Q6D216	Q6D216 erwania car
44	30	68.2	151 2 Q8ZD76	Q8ZD76 yersinia pe
45	30	68.2	151 2 AAS62716	AAS62716 yersinia

ALIGNMENTS

RESULT 1
ID Q98AR9 PRELIMINARY; PRT; 192 AA.
AC Q98AR9;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE M15880 protein.
GN Ordered locus names=ml15880;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214974;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Ideasa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.,
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti (supplement).";
RL DNA Res. 7:381-406 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Watanabe A., Ideasa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.,
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
RL DNA Res. 7:331-338 (2000).
DR EMBL: AP003007; BAB52253.1; -
DR HSP: Q9ZFY9; 1FK8.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR002198; ADH_short.
DR InterPro: IPR002347; Adh_short_C2.
DR Pfam: PF00106; adh_short_1.
DR PRINTS: PR00081; GDHRDH.
KW Complete proteome.
SQ SEQUENCE 192 AA; 20183 MW; FD2F660D156037BC CRC64;
Query Match 81.8%; Score 36; DB 2; Length 192;
Best Local Similarity 71.4%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 176 CSPATGC 182

RESULT 2

086AK7 ID 086AK7 PRELIMINARY; PRT; 360 AA.
AC 086AK7/ 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Similar to Dicyostelium discoidum (Slime mold). Prestalk protein.
OS Dicyostelium discoidum (Slime mold).
OC Eukaryota; Mycetozoa; Dicyostelidae; Dicyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910;
RA Gloeckner G., Eichinger L., Szatranski K., Pachecat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Gilgo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dicyostelium discoidum."; Nature 418:79-85(2002).
RL [2]
RN SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR HSSP; P01382; INTN.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR001673; S_mold_repeat.
DR Pfam; PF00526; Dicy_CTDc; 13.
DR PRINTS; PR00261; LDLRECEPTOR.
SQ SEQUENCE 360 AA; 3813 MW; 4B061ABA26ED81E CRC64;

Query Match Best Local Similarity 81.8%; Score 36; DB 2; Length 360; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CXPXTGC 10
Db 211 CSPSTGC 217

RESULT 3

08KU72 ID 08KU72 PRELIMINARY; PRT; 546 AA.
AC 08KU72/ 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE PUTATIVE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE PROTEIN.
GN Name=msl329;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RA7A;
RX MEDLINE=2199272; PubMed=12003951;
RA Sullivan J.T., Trzebiatowski J.R., Cruickshank R.W., Gouzy J., Brown S.D., Elliot R.M., Fleetwood D.J., McCallum N.G., Rosebach U., Stuart G.S., Weaver J.E., Webby J.J., de Bruijn F.J., Ronson C.W.;
RT "Comparative sequence analysis of the symbiosis island of Mesorhizobium loti strain RA7A." J. Bacteriol. 184:3086-3095(2002).
RL [1]
RN [1]
RC STRAIN=RA7A;
RX Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR HSSP; P50163; ZAE1.

DR GO; GO:0016491; P:oxidoreductase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002347; Adh_short_C2.
DR Pfam; PF00106; adh_short_2.
DR PRINTS; PR00081; GDRDH.
DR PROSITE; PS00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KM Oxidoreductase.
SQ SEQUENCE 546 AA; 56900 MW; 091D2EFED8E5A9C CRC64;

Query Match Best Local Similarity 81.8%; Score 36; DB 2; Length 546; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CXPXTGC 10
Db 530 CSPATGC 536

RESULT 4

07MAJ3 ID 07MAJ3 PRELIMINARY; PRT; 601 AA.
AC 07MAJ3/ 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE DIF-induced prestalk pdd63 protein precursor (Fragments).
OS Dicyostelium discoidum (Slime mold).
OC Eukaryota; Mycetozoa; Dicyostelidae; Dicyostelium.
OX NCBI_TaxID=44689;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=87187613; PubMed=3568124;
RA Williams J.G., Ceccarelli A., McRobbie S., Mahubani H., Kay R.R., Early A., Berks M., Jeremy K.A.;
RT "Direct induction of Dicyostelium prestalk gene expression by DIF Cell 49:185-192(1987).
RL Cell 49:185-192(1987).
DR FIC; A27020; A27020.
DR InterPro; IPR001673; S_mold_repeat.
DR Pfam; PF00526; Dicy_CTDc; 19.
FT NON TER 601
SQ SEQUENCE 601 AA; 63359 MW; 7D4433616CDAC438 CRC64;

Query Match Best Local Similarity 81.8%; Score 36; DB 2; Length 601; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CXPXTGC 10
Db 245 CSPSTGC 251

RESULT 5

09NO18 ID 09NO18 PRELIMINARY; PRT; 148 AA.
AC 09NO18/ 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Plimates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUES=Cerebellum cortex;
RA Osada N., Hida M., Kuroda J., Tanuma R., Iseki K., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL, AB046629, BAB03547.1; -.
KW Hypothetical protein.
SQ SEQUENCE 148 AA; 15495 MW; 6242BCE430CE613B CRC64;

Query Match 79.5%; Score 35; DB 2; Length 148;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CXPXTGC 10
| | | | |
Db 74 CGPSTGC 80

RESULT 6

095KXD2 PRELIMINARY; PRT; 148 AA.

AC 095KXD2.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Macaca.

OX NCBI_TaxID=9541;

RN [1]

RP SEQUENCE FROM N.A.

RC Tissue-Medulla oblongata;

RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,

RA Suzuki Y., Sugano S., Hashimoto K.;

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL, AB062948, BAB60737.1; -.

KM Hypothetical protein.

SQ SEQUENCE 148 AA; 15473 MW; C8D2AA301E0C8191 CRC64;

Query Match 79.5%; Score 35; DB 2; Length 148;
Best Local Similarity 71.4%; Pred. No. 33;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CXPXTGC 10
| | | | |
Db 74 CGPSTGC 80

RESULT 7

09AQP5 PRELIMINARY; PRT; 571 AA.

AC 09AQP5.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Putative ABC transporter subunit.

GN Name=ORP31;

OS Pseudomonas resinovorans.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=53412;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CA10;

RA MEDLINE=97386424; PubMed=9244273;

RA Sato S., Ouchiyama N., Kimura T., Nojiri H., Yamane H., Omori T.,

RT "Cloning of genes involved in carbazole degradation of pseudomonas sp.

RT strain CA10: nucleotide sequence of genes and characterization of

RT meta-cleavage enzymes and hydrolase.";

RL J. Bacteriol. 179:4841-4849(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CA10;

RA MEDLINE=97386425; PubMed=9244274;

RA Sato S., Nam J., Kasuga K., Nojiri H., Yamane H., Omori T.,

RT "Identification and characterization of genes encoding carbazole 1,2a-

RT dioxynase in Pseudomonas sp. strain CA10.";

RL J. Bacteriol. 179:4850-4858(1997).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=CA10;

RA MEDLINE=21264379; PubMed=11371531;

RA Nojiri H., Sekiguchi H., Maeda K., Urata M., Nakai S., Yoshida T.,

RA Habe H., Omori T.,

RT "Genetic characterization and evolutionary implications of car gene

RT cluster in carbazole-degrader, Pseudomonas sp. strain CA10.";

RL J. Bacteriol. 183:3663-3679(2001).

DR EMBL, AB047548, BAB32742.1; -.

DR GO, GO:0016020; C-membrane; IEA.

DR GO, GO:0005215; F-transporter activity; IEA.

DR GO, GO:0006810; F-transport; IEA.

DR InterPro, IPR001851; Bac_lmem_transp.

DR Pfam, PF02653; Riboosomal_S2.

DR PROSITE, PS00962; RIBOSOMAL_S2_1; UNKNOWN 1.

SQ SEQUENCE 571 AA; 60653 MW; 9A854777078C186 CRC64;

Query Match 79.5%; Score 35; DB 2; Length 571;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CXPXTGC 10
| | | | |
Db 565 CGPSTGC 571

RESULT 8

0726J7 PRELIMINARY; PRT; 113 AA.

AC 0726J7.
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RA MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares W.B., Donald M.F., Caesvarat T.L., Scheetz T.E.,

RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,

RA Krzywinski M.J., Skalska U., Smallos D.E., Scherch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RA Strausberg R.;

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL, BC053646; AAH53646.1; -.

KW Hypothetical protein.

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80 SEQUENCE 113 AA; 11613 MW; 8624A4297FAA3FF CRC64;
Query Match 77.3%; Score 34; DB 2; Length 113;
Best Local Similarity 71.4%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 4 CXPXTGC 10
| | | |
Db 103 CYPKTGC 109

RESULT 9
PA2X_NOTSC STANDARD; PRT; 145 AA.
AC P20146;
DT 01-PEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Probable phospholipase A2 precursor (EC 3.1.1.4) (Phosphatidylcholine
DE 2-acetylglucolase).
OS Notochis scutatus scutatus (Mainland tiger snake) (Common tiger
OS snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acantophiinae; Notochis.
OX NCBI_TaxID=70142;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=venom gland;
RA Duncanel P.;
RL Submitted (JAN-1989) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a carboxylate.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the phospholipase A2 family. Group I
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL, X14043; CAA32201.1; -.
DR PIR, S07983; S07983.
DR HSBP, P00606; 1AE7.
DR InterPro, IPR001211; PhospholipaseA2.
DR Pfam, PF00068; Phospholip_A2_1; 1.
DR PRINTS, PR00389; PPHPLPASEA2.
DR Prodom, PD000303; PhospholipaseA2; 1.
DR SMART, SM00085; PA2c; 1.
DR PROSITE, PS00119; PA2_ASP; 1.
DR PROSITE, PS00118; PA2_HIS; 1.
KW Calcium; Hydrolyase; Lipid degradation; Multigene family; Signal.
FT SIGNAL 1 21 Potential.
FT PROPEP 22 27 Potential.
FT CHAIN 28 145 Probable phospholipase A2.
FT ACT_SITE 75 75 By similarity.
FT ACT_SITE 119 119 By similarity.
FT DISULFID 38 98 By similarity.
FT DISULFID 54 144 By similarity.
FT DISULFID 56 72 By similarity.
FT DISULFID 71 125 By similarity.
FT DISULFID 78 118 By similarity.
FT DISULFID 87 111 By similarity.
FT DISULFID 105 116 By similarity.
FT METAL 55 55 Calcium (via carbonyl oxygen) (By
FT similarity).

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FT	METAL	57	57	Calcium (via carbonyl oxygen) (By similarity).
FT	METAL	76	76	Calcium (By similarity).
SQ	SEQUENCE	145 AA;	16002 MW;	3BE35029AEB5FAC9 CRC64;
	Query Match			
	Best Local Similarity	77.3%;	Score 34;	DB 1; Length 145;
	Matches . 5;	Conservative	0;	Mismatches 2; Indels 0; Gaps 0;
OY	4 CXPXTGC 10			
Db	105 CDPEPTGC 111			
	RESULT 10			
ID	Q7U7V9	PRELIMINARY;	PRT;	167 AA.
AC	Q7U7V9;			
DT	01-OCT-2003 (TREMBlrel. 25, Created)			
DT	01-OCT-2003 (TREMBlrel. 25, Last sequence update)			
DE	Hypothetical precursor.			
CN	OrderedLocustNames=SYNM0871;			
OS	Synechococcus sp. (strain WH8102).			
OC	Bacteria; Cyanobacteria; Chroococcales; Synechococcus.			
OX	NCB1_TaxID=84588;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=228256597; PubMed=12917641; DOI=10.1038/nature01943;			
RA	PatentK B., Brahmsma B., Larimer F.W., Land M.L., Hauser L.,			
RA	Chaitin F., Lanezrdin J.E., Regala W., Allen R.E., McCarren J.,			
RA	Paulsen I.T., Dutreine A., Pattersky F., Webb E.A., Waterbury J.;			
RL	"The genome of a motile marine Synechococcus".			
DR	Nature 424:1037-1042(2003).			
KW	EMBL; BX565691; CAE07386.1; "			
FT	Complete proteome; Hypothetical protein; Signal.			
SQ	SIGNAL 1			
	POTENTIAL 22			
	SEQUENCE 167 AA;			
	18419 MW;			
	OB3AFB830BCFP971C CRC64;			
	Query Match			
	Best Local Similarity	77.3%;	Score 34;	DB 2; Length 167;
	Matches 5;	Conservative	0;	Mismatches 2; Indels 0; Gaps 0;
OY	4 CXPXTGC 10			
Db	133 CYPGTGC 139			
	RESULT 11			
ID	O9SUJ3	PRELIMINARY;	PRT;	312 AA.
AC	O9SUJ3;			
DT	01-MAY-2000 (TREMBlrel. 13, Created)			
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)			
DE	05-JUL-2004 (TREMBlrel. 27, Last annotation update)			
CN	Hypothetical protein FB84.80 (Hypothetical protein ATg32380).			
GN	Name=FB84.80; Synonyms=ATg32380;			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Bevan M., Terry N., Ardiles W., Buysheart C., Dasseville R.,			
RA	De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,			
RA	Villareel R., Glisen U., Van Montagu M., Hohenseil U., Mewes H.W.,			
RA	Mayer K.F.X., Lemcke K., Schueller C.;			
RL	Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RA	EU Arabidopsis sequencing project;			
RL	Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.			

```

RN [3]
RP SEQUENCE FROM N.A.
RA Terry N., Ardiles W., Buysheart C., Dasseville R., De Clerck R.,
RA De Kuyser A., Neyt P., Rouze P., Van Den Daele H., Villarroel R.,
RA Gielens J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
DR EMBL; AL034567; CAZ2255.1; -.
DR PIR; T05348; T05348.
DR GO; GO:0004650; P:polysaccharonase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR000743; Glyco_hydro_28.
DR InterPro; IPR006625; Pbh1.
DR InterPro; IPR011050; Pectin_lyase.
DR Pfam; PF00295; Glyco_hydro_28; 2.
DR SMART; SM00710; Pbh1; 3.
KM Cell wall, Glycosidase; Hydrolyase; Hypothetical protein.
SQ SEQUENCE 312 AA; 34095 MW; E2E70A2622F30E80 CRC64;

Query Match 77.3%; Score 34; DB 2; Length 312;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CXPXTC 10
DB 208 CDPPTGC 214

RESULT 12
O6TVH9 PRELIMINARY; PRT; 465 AA.
ID O6TVH9
AC OCTVH9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Bovine papular stomatitis virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Parapoxvirus.
OC NCBI_TaxID=129727;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=BY-AR02;
RX PubMed=14671098;
RA Delhon G., Tulman E.R., Afonso C.L., Lu Z., Piccone M.E., Kutish G.F.,
RA de la Concha-Bermejo A., Lehmkuhl H.D., Piccone M.E., Kutish G.F.,
RA Rock D.L.;
RA "Genomes of the Parapoxviruses Orf Virus and Bovine Papular
RT Stomatitis Virus";
RL J. Virol. 78:168-177(2004).
DR EMBL; AY386265; AAR98366.1; -.
DR InterPro; IPR007027; Pox_F1.
DR Pfam; PF04943; Pox_F1; 1.
KM Hypothetical protein.
SQ SEQUENCE 465 AA; 51404 MW; BD735469CBED1B79 CRC64;

Query Match 77.3%; Score 34; DB 2; Length 465;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CXPXTC 10
DB 26 CVPPTGC 32

RESULT 13
AAR98366 PRELIMINARY; PRT; 465 AA.

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AC AAR98366;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Bovine papular stomatitis virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Parapoxvirus.
OC NCBI_TaxID=129727;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=BY-AR02;
RX PubMed=14671098;
RA Delhon G., Tulman E.R., Afonso C.L., Lu Z., Piccone M.E., Kutish G.F.,
RA de la Concha-Bermejo A., Lehmkuhl H.D., Piccone M.E., Kutish G.F.,
RA Rock D.L.;
RA "Genomes of the Parapoxviruses Orf Virus and Bovine Papular
RT Stomatitis Virus";
RL J. Virol. 78:168-177(2004).
DR EMBL; AY386265; AAR98366.1; -.
KM Hypothetical protein.
SQ SEQUENCE 465 AA; 51404 MW; BD735469CBED1B79 CRC64;

Query Match 77.3%; Score 34; DB 2; Length 465;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CXPXTC 10
DB 26 CVPPTGC 32

RESULT 14
Q8LJ36 PRELIMINARY; PRT; 574 AA.
ID Q8LJ36
AC Q8LJ36;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE P0413G02.18 protein.
GN Name=P0413G02.18;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OC NCBI_TaxID=39947;
OX [1]
RN SEQUENCE FROM N.A.
RP Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nishimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Naito N., Negishi M., Ohta I., Ono N., Saij S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Zhao M., Jiang J., Golobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AF003344; BAC07361.1; -.
DR HSSP; P20142; IAVF.
DR Gramene; Q8LJ36; -.
DR GO; GO:0004194; F:pepsin A activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001461; Peptidase_A1.
DR InterPro; IPR005007; Pept_Aspartic.
DR Pfam; PF00026; Asp; 1.
DR PRINTS; PR00792; PEPSIN.

```

SEQ SEQUENCE 574 AA; 60980 MW; A2D654446084F35F CRC64;

Query Match 77.3%; Score 34; DB 2; Length 574;
 Best Local Similarity 71.4%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CXPXTC 10
 | | | |
 Db 119 CSPCTGC 125

RESULT 15

Q869K4 PRELIMINARY; PRT; 998 AA.
 ID Q869K4
 AC Q869K4
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Similar to Mus musculus (mouse). Tenascin X.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 CX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA MEDLINE=22092622; PubMed=12097910;
 RA Gloeckner G., Eichinger L., Szatranek K., Pachebat J., Dear P.,
 RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
 RA Turguel B., Cox B., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.,
 RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."/
 RL Nature 418:79-85(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA Baumgart C.,
 RL Submitted (MAR-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AC115598; AAO53206.1; -
 DR HBBP; P01132; IEGF.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR006209; EGF_1like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR002049; Laminin_EGF.
 DR Pfam; PF00008; EGF; 7.
 DR PRINTS; PR00011; EGF/LAMININ.
 DR SMART; SM00181; EGF; 9.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_10.
 DR PROSITE; PS01186; EGF_2; 7.
 DR PROSITE; PS50026; EGF_3; 6.
 SQ SEQUENCE 998 AA; 106001 MW; F79BEF394D3E2369 CRC64;

Query Match 77.3%; Score 34; DB 2; Length 998;
 Best Local Similarity 71.4%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CXPXTC 10
 | | | |
 Db 609 CNPFTGC 615

Search completed: January 12, 2005, 23:15:11
 Job time : 168.45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2005, 23:04:08 ; Search time 31.2 Seconds
(without alignments)
40.090 Million cell updates/sec

Title: US-09-932-322-1

Perfect score: 44
Sequence: 1 XXXCXPTGCKXX 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	36	81.8	601 2 A27020	DIF-induced presta
2	34	77.3	145 2 S07983	phospholipase A2 h
3	34	77.3	312 2 T05348	hypothetical prote
4	33	75.0	1058 2 T50496	hypothetical prote
5	32	72.7	64 2 P96006	hypothetical prote
6	31	70.5	482 2 T48397	S-receptor kinase
7	31	70.5	643 2 T25473	hypothetical prote
8	30	68.2	129 2 A24255	chorion class A pr
9	30	68.2	132 2 B24255	chorion class A pr
10	30	68.2	151 2 AB0331	sigma E factor reg
11	30	68.2	199 2 T49486	hypothetical prote
12	30	68.2	200 2 S04526	wound-induced prot
13	30	68.2	201 2 T07729	wound-induced prot
14	30	68.2	211 2 T04098	CBP20 preproprote
15	30	68.2	211 2 S04927	wound-induced prot
16	30	68.2	222 1 MWVZB4	anti-thrombin-III h
17	30	68.2	224 2 R84326	hypothetical prote
18	30	68.2	336 2 A83801	ABC transporter (s
19	30	68.2	345 1 MWVZM2	anti-thrombin-III h
20	30	68.2	406 2 T23898	hypothetical prote
21	30	68.2	430 2 T23899	hypothetical prote
22	30	68.2	551 2 S01793	arylsulfatase (EC
23	30	68.2	551 2 S07089	arylsulfatase (EC
24	30	68.2	648 2 T23864	hypothetical prote
25	30	68.2	1722 2 E89753	protein P11C7.4 [I
26	29	65.9	46 2 H71262	hypothetical prote
27	29	65.9	119 2 B45937	early chorion prot
28	29	65.9	119 2 S24292	chorion protein -
29	29	65.9	119 2 S24294	chorion protein -

30	29	65.9	119 2 S24291	chorion protein -
31	29	65.9	121 2 S24293	chorion class CA p
32	29	65.9	147 2 B82523	hypothetical prote
33	29	65.9	163 2 T33130	hypothetical prote
34	29	65.9	245 2 F84680	hypothetical prote
35	29	65.9	333 2 P90172	hypothetical prote
36	29	65.9	348 2 T15248	probable oxidoredu
37	29	65.9	375 2 A83636	hypothetical prote
38	29	65.9	379 2 S14885	hypothetical prote
39	29	65.9	449 2 B96676	hypothetical prote
40	29	65.9	507 2 T23375	hypothetical prote
41	29	65.9	513 2 D88991	protein apx-1 [imp
42	29	65.9	685 2 JC7570	Delta-4 protein -
43	29	65.9	686 2 UC7569	hypothetical prote
44	29	65.9	753 2 T28787	complement C7 prec
45	29	65.9	843 1 A27340	

ALIGNMENTS

RESULT 1
A27020
DIF-induced prestalk pdd3 protein precursor - slime mold (Dictyostelium discoideum) (E
C:Species: Dictyostelium discoideum
C>Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C/Accession: A27020
R:Williams, J.G.; Caccarelli, A.; McRobbie, S.; Mahbubani, H.; Kay, R.R.; Early, A.; Be
Cell 49, 185-192, 1987
A>Title: Direct induction of Dictyostelium prestalk gene expression by DIF provides evi
A/Reference number: A27020; MUID:87187613; PMID:3568124
A/Accession: A27020
A/Molecule type: DNA
A/Residues: 1-601 <MTL>
A/Cross-references: UNIPROT:Q7M4J3
C/Genetics:
A/Name: PDD63
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-601/Product: DIF-induced prestalk pdd3 protein #status predicted <MAT>

Query Match 81.8%; Score 36; DB 2; Length 601;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CXPTGC 10
DB 245 CSPSTGC 251

RESULT 2
S07983
phospholipase A2 homolog precursor - common tiger snake
C/Species: Notocheilus scutatus scutatus (common tiger snake)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C/Accession: S07983
R/Duncan, J. F.
submitted to the EMBL Data Library, January 1989
A/Reference number: S07983
A/Accession: S07983
A/Molecule type: mRNA
A/Residues: 1-145 <DUC>
A/Cross-references: UNIPROT:P20146; EMBL:X14043; NID:G64109; PIDN:CA32201.1; PID:G6411
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-145/Product: phospholipase A2 #status predicted <MAT>

Query Match 77.3%; Score 34; DB 2; Length 145;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CXPTGC 10
DB 105 CSPSTGC 111

RESULT 3

T05348
 hypothetical protein F8B4.80 - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C/Accession: T05348
 R/Bevan, M.; Terry, N.; Ardiles, W.; Buyssehaert, C.; Dasseville, R.; De Clerck, R.; De ewes, H.W.; Mayer, K.F.X.; Schaeffer, C.
 submitted to the Protein Sequence Database, February 1999
 A/Reference number: 215409
 A/Accession: T05348
 A/Molecule type: DNA
 A/Residues: 1-312 <BEV>
 A/Cross-references: UNIPROT:Q98UV3; EMBL:AL034567
 A/Experimental source: cultivar Columbia; BAC clone F8B4
 C/Genetics:
 A/Map position: 4
 A/Intons: 1/3; 44/3; 101/3; 139/3; 180/3
 A/Note: F8B4.80

Query Match 77.3%; Score 34; DB 2; Length 312;
 Best Local Similarity 71.4%; Pred. No. 32;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CXPYTC 10
 Db 208 CDPYTC 214

RESULT 4

T50496
 hypothetical protein T22D6.50 - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
 C/Accession: T50496
 R/Bevan, M.; Terry, N.; Ardiles, W.; Buyssehaert, C.; Dasseville, R.; De ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, May 2000
 A/Reference number: 225101
 A/Accession: T50496
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-1058 <BEV>
 A/Cross-references: UNIPROT:Q9LZS5; EMBL:AL357612
 A/Experimental source: cultivar Columbia; BAC clone T22D6
 C/Genetics:
 A/Map position: 5
 A/Intons: 60/3; 195/3; 222/3; 448/3; 492/3; 526/3; 555/2; 591/2; 616/3; 662/2; 715/3; 7
 A/Note: T22D6.50

Query Match 75.0%; Score 33; DB 2; Length 1058;
 Best Local Similarity 71.4%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CXPYTC 10
 Db 1019 CDPYTC 1025

RESULT 5

F96006
 hypothetical protein (imported) - Sinorhizobium meliloti (strain 1021) megaplasmid pSymB
 C/Species: Sinorhizobium meliloti
 C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C/Accession: F96006
 R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernat Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A/Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc
 A/Reference number: A95842; MUID:21396508; PMID:11481431
 A/Accession: F96006
 A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-64 <KUR>
 A/Cross-references: UNIPROT:Q92U25; GB:AL591985; PIDN:CAC49718.1; PID:G15141205; GSPDB: R/Galibert, P.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler pel, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F. L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kise, E.; Komp, C.; lelaure hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K
 A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A/Reference number: A96039; MUID:21368234; PMID:11474104
 A/Contents: annotation
 C/Genetics:
 A/Gene: SMD21688
 A/Genome: plasmid

Query Match 72.7%; Score 32; DB 2; Length 64;
 Best Local Similarity 57.1%; Pred. No. 22;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 CXPYTC 10
 Db 15 CAPSSGC 21

RESULT 6

T48397
 S-receptor kinase-like protein - Arabidopsis thaliana
 N/Alternate names: protein F17C15.120
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C/Accession: T48397
 R/Bevan, M.; Pohl, T.; Welzenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.
 submitted to the Protein Sequence Database, March 2000
 A/Reference number: 224492
 A/Accession: T48397
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-482 <BEV>
 A/Cross-references: UNIPROT:Q9LZR8; EMBL:AL162506
 A/Experimental source: cultivar Columbia; BAC clone F17C15
 C/Genetics:
 A/Map position: 5
 A/Note: F17C15.120

Query Match 70.5%; Score 31; DB 2; Length 482;
 Best Local Similarity 57.1%; Pred. No. 1.6e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 CXPYTC 10
 Db 301 CTPSSGC 307

RESULT 7

T25473
 hypothetical protein B0507.1 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T25473
 R/Bradshaw, H.
 submitted to the EMBL Data Library, July 1996
 A/Description: The sequence of C. elegans cosmid B0507.
 A/Reference number: Z20039
 A/Accession: T25473
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-643

 A/Cross-references: UNIPROT:Q22886; EMBL:U64833; PIDN:AA04822.1; GSPDB:GN00023; CESP: B
 A/Experimental source: strain Bristol N2; clone B0507
 C/Genetics:
 A/Gene: CESP:B0507.1

A/Map position: 5
A/Introns: 59/3; 133/1; 464/3; 586/1

Query Match 70.5%; Score 31; DB 2; Length 643;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CXPXTGC 10
DB 209 CXPXTGC 215

RESULT 8

B24255
Chorion class A protein L11 precursor - silkworm

C/Species: Bombyx mori (silkworm)
C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004

C/Accession: A24255

R/Spoerel, N.; Nguyen, H.T.; Kafatos, F.C.

J. Mol. Biol. 190, 23-35, 1986

A/Title: Gene regulation and evolution in the chorion locus of Bombyx mori. Structural
A/Reference number: A92929; PMID:87060979; PMID:3023635

A/Accession: A24255

A/Molecule type: DNA

A/Residues: 1-129 <SPO>

A/Cross-references: UNIPROT: P08826; GB: X15557; GB: X04028; GB: X04029; GB: X04030; GB: X0403

C/Superfamily: Chorion class A protein pc292

F/1-21/Domain: signal sequence #status predicted <SIG>

F/22-129/Product: chorion class A protein L11 #status predicted <MAT>

Query Match 68.2%; Score 30; DB 2; Length 129;
Best Local Similarity 57.1%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CXPXTGC 10
DB 116 CAPTGC 122

RESULT 9

B24255
Chorion class A protein L12 precursor - silkworm

C/Species: Bombyx mori (silkworm)

C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004

C/Accession: B24255

R/Spoerel, N.; Nguyen, H.T.; Kafatos, F.C.

J. Mol. Biol. 190, 23-35, 1986

A/Title: Gene regulation and evolution in the chorion locus of Bombyx mori. Structural
A/Reference number: A92929; PMID:87060979; PMID:3023635

A/Accession: B24255

A/Molecule type: DNA

A/Residues: 1-132 <SPO>

A/Cross-references: UNIPROT: P08825; GB: X15557; GB: X04028; GB: X04029; GB: X04030; GB: X0403

C/Superfamily: Chorion class A protein pc292

F/1-21/Domain: signal sequence #status predicted <SIG>

F/22-132/Product: chorion class A protein L12 #status predicted <MAT>

Query Match 68.2%; Score 30; DB 2; Length 132;
Best Local Similarity 57.1%; Pred. No. 90;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CXPXTGC 10
DB 117 CAPTGC 123

RESULT 10

AB0331
sigma E factor regulatory protein rsec [imported] - Yersinia pestis (strain C092)

C/Species: Yersinia pestis

C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C/Accession: AB0331

R/Perkhill, J.; Wren, B.W.; Thomson, N.R.; Tlball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11; M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, L.

Nature 413, 523-527, 2001

A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A/Reference number: AB0001; PMID:21470413; PMID:11586360

A/Accession: AB0331

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-151 <KUR>

A/Cross-references: UNIPROT: Q82D76; GB: AL590842; PIDN: CAC92953.1; PID: G15980692; GSPDB:

C/Genetics:

A/Gene: rsec

C/Superfamily: Escherichia coli sigma-E factor regulatory protein rsec

Query Match 68.2%; Score 30; DB 2; Length 151;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CXPXTGC 10
DB 20 CXPXTGC 26

RESULT 11

T49486
Hypothetical protein B14D6.380 [imported] - Neurospora crassa

C/Species: Neurospora crassa

C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000

C/Accession: T49486

R/Schulte, U.; Aign, V.; Hohenisel, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura

submitted to the Protein Sequences Database, May 2000

A/Reference number: Z25022

A/Accession: T49486

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-199 <SCH>

A/Cross-references: EMBL: AL356173; GSPDB: GN00116; NCSP: B14D6.380.

A/Experimental source: BAC clone B14D6; strain OR74A

C/Genetics:

A/Gene: NCSP: B14D6.380

A/Map position: 6

C/Superfamily: Neurospora crassa hypothetical protein B14D6.380

Query Match 68.2%; Score 30; DB 2; Length 199;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CXPXTGC 10
DB 155 CXPXTGC 161

RESULT 12

S04926
Wound-induced protein 1 precursor - potato

C/Species: Solanum tuberosum (potato)

C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004

C/Accession: S04926

R/Stanford, A.; Bevan, M.; Northcote, D.

Mol. Gen. Genet. 215, 200-208, 1989

A/Title: Differential expression within a family of novel wound-induced genes in potato

A/Reference number: S04926; PMID:89218921; PMID:2710099

A/Accession: S04926

A/Molecule type: DNA

A/Residues: 1-200 <STA>

A/Cross-references: UNIPROT: P09761; EMBL: X13497; NID: G21617; PIDN: CAA31851.1; PID: G2161

C/Genetics:

A/Introns: 143/3

C/Superfamily: hevein precursor; barwin homology; hevein chitin-binding domain homology

F/1-25/Domain: signal sequence #status predicted <SIG>

F/26-200/Product: wound-induced protein 1 #status predicted <MAT>

F/26-69/Domain: hevein chitin-binding domain homology <HCB>

F:78-199/Domain: barwin homology <BAR>

Query Match

Best Local Similarity 68.2%; Score 30; DB 2; Length 200;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CXPXTGC 10
DB 56 CSPSQGC 62

RESULT 13

T07729

wound-induced protein (clone TAB7) - tomato (fragment)

C/Species: Lycopersicon esculentum (tomato)

C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004

C/Accession: T07729

R/Harris, N.; Taylor, J.E.; Roberts, J.A.

J. Exp. Bot. 48, 1223-1227, 1997

A/Title: Characterization and expression of an mRNA encoding a wound-induced (win) prote

A/Reference number: 216099

A/Accession: T07729

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-201 <HAR>

A/Cross-references: UNIPROT:O03994; EMBL:U89764; NID:g1888560; PIDN:AA849688.1; PID:g188

A/Experimental source: strain A15a cralg; leaf abscission zone tissue

C/Superfamily: hevein precursor; barwin homology; hevein chitin-binding domain homology

F:16-60/Domain: hevein chitin-binding domain homology <HCB>

F:68-188/Domain: barwin homology <BAR>

Query Match

Best Local Similarity 68.2%; Score 30; DB 2; Length 201;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CXPXTGC 10
DB 46 CSPSQGC 52

RESULT 14

T04098

CBP20 preproprotein - common tobacco

N/Alternate names: wound-induced protein

C/Species: Nicotiana tabacum (common tobacco)

C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C/Accession: T04098

R/Ponstein, A.S.; Bree-Vloemans, S.A.; Sela-Buurlage, M.B.; Elzen, P.J.; Melchers, L.S.;

Plant Physiol. 104, 109-118, 1994

A/Title: A novel pathogen- and wound-inducible tobacco (Nicotiana tabacum) protein with

A/Reference number: 215209; MUID:94159785; PMID:8115541

A/Accession: T04098

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-211 <PON>

A/Cross-references: UNIPROT:Q41231; EMBL:S72452; NID:g632733; PIDN:AA829959.1; PID:g6327

A/Experimental source: cultivar Samun NN

C/Superfamily: hevein precursor; barwin homology; hevein chitin-binding domain homology

F:23-66/Domain: hevein chitin-binding domain homology <HCB>

F:78-199/Domain: barwin homology <BAR>

Query Match

Best Local Similarity 68.2%; Score 30; DB 2; Length 211;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CXPXTGC 10
DB 53 CSPSQGC 59

RESULT 15

S04927

wound-induced protein 2 precursor - potato

C/Species: Solanum tuberosum (potato)

C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004

C/Accession: S04927

R/Stanford, A.; Bevan, M.; Northcote, D.

Mol. Gen. Genet. 215, 200-208, 1989

A/Title: Differential expression within a family of novel wound-induced genes in potato

A/Reference number: S04926; MUID:89218921; PMID:2710099

A/Accession: S04927

A/Molecule type: DNA

A/Residues: 1-211 <STA>

A/Cross-references: UNIPROT:P09762; EMBL:X13497; NID:g21617; PIDN:CAA31852.1; PID:g2161

C/Genetics:

A/Gene: win2

A/Insertions: 142/3

C/Superfamily: hevein precursor; barwin homology; hevein chitin-binding domain homology

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-211/Product: wound-induced protein 2 #status predicted <MAT>

F:26-69/Domain: hevein chitin-binding domain homology <HCB>

F:77-198/Domain: barwin homology <BAR>

Query Match

Best Local Similarity 68.2%; Score 30; DB 2; Length 211;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CXPXTGC 10
DB 56 CSPSQGC 62

Search completed: January 12, 2005, 23:16:03
Job time : 33.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2005, 22:55:47 ; Search time 146.9 Seconds
(without alignments)
31.746 Million cell updates/sec

Title: US-09-932-322-1
Perfect score: 44
Sequence: 1 XXXCKPXTGCKXX 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_238ep04:*

- 1: geneseqp19808:*
- 2: geneseqp19908:*
- 3: geneseqp20008:*
- 4: geneseqp20018:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
- 7: geneseqp20048:*
- 8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	35	79.5	79	AAU9413 Propionib
2	35	79.5	79	ABM45932 Propionib
3	35	79.5	180	ABO74428 Pseudomon
4	34	77.3	7	AAV62764 PB-cadher
5	34	77.3	7	AAV61489 Cadherin-
6	34	77.3	7	AAV62007 Cadherin-
7	34	77.3	7	AAV62224 Cadherin-
8	34	77.3	7	ABJ00550 B lymphoc
9	34	77.3	7	ABG33862 B lymphoc
10	34	77.3	13	ABJ00545 B lymphoc
11	34	77.3	13	ABG33861 B lymphoc
12	34	77.3	53	AAU44932 Propionib
13	34	77.3	53	ABM41451 Propionib
14	34	77.3	113	ADA54961 Human pro
15	34	77.3	128	ABM42027 Human ORF
16	34	77.3	250	ABO75329 Pseudomon
17	34	77.3	312	ABB93198 Herbicida
18	34	77.3	540	ADP05702 Bacterial
19	34	77.3	3226	ABG28408 Novel hum
20	33	75.0	158	AAU40006 Propionib
21	33	75.0	158	ABM36525 Propionib
22	32	72.7	751	ABM36526 Arabidops
23	32	72.7	798	AAU43625 Arabidops
24	32	72.7	835	AAU43624 Arabidops
25	31	70.5	7	AAV63264 Protocad

26	31	70.5	90	ABO81251 Pseudomon
27	31	70.5	114	ABP06368 Human ORF
28	31	70.5	148	ADJ71040 Human hea
29	31	70.5	183	ADF58925 Human pol
30	31	70.5	193	AAO00015 Human pol
31	31	70.5	193	ADF60298 Human con
32	31	70.5	238	ABP99259 Orthosomy
33	31	70.5	239	ABP99348 Orthosomy
34	31	70.5	239	ABP76713 Streptomycin
35	31	70.5	310	ABO74638 Pseudomon
36	31	70.5	444	ABO70819 Pseudomon
37	31	70.5	482	ABB93340 Herbicida
38	31	70.5	580	AAW32363 Mycobacte
39	31	70.5	580	AAW32431 Mycobacte
40	31	70.5	580	AAW64303 Mycobacte
41	31	70.5	580	AAW81666 M. tuberc
42	31	70.5	580	AAV38968 M. tuberc
43	31	70.5	580	AAV39105 M. tuberc
44	31	70.5	602	AAV04996 Mycobacte
45	31	70.5	638	AAV04992 Mycobacte

ALIGNMENTS

RESULT 1
AAU9413 standard; protein; 79 AA.
AAU9413; (first entry)
13-FEB-2002
Propionibacterium acnes immunogenic protein #10309.
SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
Propionibacterium acnes.
WO200181581-A2.
01-NOV-2001.
20-APR-2001; 2001WO-US012865.
21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
(CORI-) CORIXA CORP.
Skelky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A; L'Waissonneuve J, Zhang Y, Jen S, Carter D; N-PSDB; AAS59545.
Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
Example 1; SEQ ID NO 10608; 1069pp; English.
Sequences AAU9105-AAU6801 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory

lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 79 AA:

Query Match 79.5%; Score 35; DB 4; Length 79;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CXPXTC 10
Db 3 CSPETGC 9

RESULT 2

ABM45932 standard; protein; 79 AA.

ABM45932;

20-OCT-2003 (first entry)

Propionibacterium acnes predicted ORF-encoded polypeptide #10608.

Acne vulgaris; antiseborrheic; dermatological; antibacterial;
immunostimulant; immune response; vaccine.

Propionibacterium acnes.

WO2003033515-A1.

24-APR-2003.

11-OCT-2002; 2002WO-US032727.

15-OCT-2001; 2001US-00978825.

(CORI-) CORIAX CORP.

Mitcham JL, Skelky YAN, Persing DH, Bhatia A, Maisonneuve JL;
Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
Barth B, Valliave-Douglas J;

WPI: 2003-381789/36.

N-PSDB; ACF64474.

New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.

Example 1, SEQ ID NO 10608; 1481bp; English.

The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention; antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides,

polynucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polynucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 79 AA:

Query Match 79.5%; Score 35; DB 6; Length 79;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CXPXTC 10
Db 3 CSPETGC 9

RESULT 3

ABO74428 standard; protein; 180 AA.

ABO74428;

29-JUL-2004 (first entry)

Pseudomonas aeruginosa polypeptide #6603.

Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

Pseudomonas aeruginosa.

US6551795-B1.

22-APR-2003.

18-FEB-1999; 99US-00252991.

18-FEB-1998; 98US-0074788P.

27-JUL-1998; 98US-0094190P.

(GENO-) GENOME THERAPEUTICS CORP.

Rubinfeld MJ, Nolling J, Deloughery C, Bueh D;

WPI: 2003-615309/58.

N-PSDB; ABD07999.

Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.

Disclosure; SEQ ID NO 23174; 455bp; English.

The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant

production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html

Sequence 180 AA;

Query Match 79.5%; Score 35; DB 7; Length 180;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

4 CXPXTGC 10
124 CRPATGC 130

RESULT 4
AA62764
ID AA62764 standard; peptide; 7 AA.

AA62764;

02-MAR-2000 (first entry)

PB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:4047.

Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin; protocadherin; cadherin related neuronal receptor; LI-cadherin; protocadherin; desmoglein; desmocollin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.

Synthetic.

Homo sapiens.

Key Location/Qualifiers

Disulfide-bond 1..7

MO9957149-A2.

11-NOV-1999.

05-MAY-1999; 99MO-CA000363.

05-MAY-1998; 98US-00073040.

06-NOV-1998; 98US-00187859.

20-JAN-1999; 99US-00234395.

08-MAR-1999; 99US-00264516.

(ADHE-) ADHEREX TECHNOLOGIES INC.

Blaschuk OW, Gour BJ, Byers S;

WPI, 2000-038791/03.

New cadherin modulating agents, used for modulating nonclassical cadherin mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.

Claim 72; Page 193; 252pp; English.

The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MA can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a

mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-expressing cell, preventing or treating obesity in a mammal, stimulating blood vessel regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal, enhancing adhesion of nonclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. CC AA60592 to AA64572 represent specifically claimed peptides, and CC AA64573 to AA64643 and AA233183 to AA233186 represent sequences used in the exemplification of the present invention

Sequence 7 AA;

Query Match 77.3%; Score 34; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

4 CXPXTGC 10
1 CDPKTC 7

RESULT 5
AA61489
ID AA61489 standard; peptide; 7 AA.

AA61489;

02-MAR-2000 (first entry)

Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1375.

Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin; protocadherin; cadherin related neuronal receptor; LI-cadherin; protocadherin; desmoglein; desmocollin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.

Synthetic.

Homo sapiens.

Key Location/Qualifiers

Disulfide-bond 1..7

MO9957149-A2.

11-NOV-1999.

05-MAY-1999; 99MO-CA000363.

05-MAY-1998; 98US-00073040.

06-NOV-1998; 98US-00187859.

20-JAN-1999; 99US-00234395.

08-MAR-1999; 99US-00264516.

(ADHE-) ADHEREX TECHNOLOGIES INC.

Blaschuk OW, Gour BJ, Byers S;

WPI, 2000-038791/03.

New cadherin modulating agents, used for modulating nonclassical cadherin

PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX
 PS Claim 36; Page 172; 252pp; English.

XX The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MA can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC -related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY6592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
 CC the exemplification of the present invention

80 Sequence 7 AA;

Query Match 77.3%; Score 34; DB 3; Length 7;
 Best Local Similarity 71.4%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CXPXTGC 10
 DB 1 CDPKTC 7

RESULT 6

AAY62007 standard; peptide; 7 AA.

XX AAY62007;

02-MAR-2000 (first entry)

DE Cadherin-12 cell adhesion recognition cyclic peptide SEQ ID NO:11799.

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.

OS Synthetic.
 OS Homo sapiens.

XX Key Location/Qualifiers

FT Disulfide-bond 1..7

XX WO957149-A2.

PD 11-NOV-1999.

XX 05-MAY-1999; 99WO-CA000363.

XX 05-MAY-1998; 98US-00073040.

PR 06-NOV-1998; 98US-00187859.

PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuk OW, Gour BJ, Byers S;
 XX WPI; 2000-038791/03.

XX New cadherin modulating agents, used for modulating nonclassical cadherin
 PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX
 PS Claim 48; Page 180; 252pp; English.

XX The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MA can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC -related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY6592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
 CC the exemplification of the present invention

80 Sequence 7 AA;

Query Match 77.3%; Score 34; DB 3; Length 7;
 Best Local Similarity 71.4%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CXPXTGC 10
 DB 1 CDPKTC 7

RESULT 7

AAY62224 standard; peptide; 7 AA.

XX AAY62224;

02-MAR-2000 (first entry)

DE Cadherin-14 cell adhesion recognition cyclic peptide SEQ ID NO:3971.

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.

OS Synthetic.
 OS Homo sapiens.

XX Key Location/Qualifiers

FT Disulfide-bond 1. 7
XX
XX MO9957149-A2.
XX 11-NOV-1999.
XX
XX 05-MAY-1999; 99WO-CA000363.
XX
XX 05-MAY-1998; 98US-00073040.
XX 06-NOV-1998; 98US-00187859.
XX 20-JAN-1999; 99US-00234395.
XX 08-MAR-1999; 99US-00254516.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blachuk OW, Gour BJ, Byers S;
XX WPI; 2000-038791/03.
XX
XX New cadherin modulating agents, used for modulating nonclassical cadherin
XX -mediated functions for treating e.g. cancers, obesity, rheumatoid
XX arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
XX Claim 54; Page 184; 252pp; English.
XX
XX The present invention describes cadherin modulating agents (MA)
XX comprising peptides which comprise a nonclassical cadherin cell adhesion
XX recognition (CAR) sequence. The MAs can be used for modulating
XX nonclassical cadherin-mediated functions. They can be used for e.g.
XX inhibiting adhesion of nonclassical-cadherin expressing cells in a
XX mammal, enhancing delivery of a drug through the skin of a mammal,
XX enhancing delivery of a drug to a tumour in a mammal, treating cancer in
XX a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
XX angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
XX expressing cell, preventing or treating obesity in a mammal, stimulating
XX blood vessel regression in a mammal, enhancing drug delivery to the
XX central nervous system, treating a demyelinating neurological disease,
XX increasing vasopermeability in a mammal, enhancing adhesion of
XX nonclassical cadherin-expressing cells, inhibiting synaptic stability in
XX a mammal, or preventing pregnancy in a mammal. They can also be used for
XX e.g. enhancing or directing neurite outgrowth, facilitating wound healing
XX or reducing scar tissue, or enhancing adhesion of foreign tissue in a
XX mammal. They can also be used for treating e.g. psoriasis, arthritis, age
XX -related macular degeneration, multiple sclerosis and diabetes. The
XX products can also be used for detection and diagnosis and in bioreactors.
XX AAY60592 to AAY64572 represent specifically claimed peptides, and
XX AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
XX the exemplification of the present invention
XX
XX Sequence 7 AA;
SQ
Query Match 77.3%; Score 34; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CXPXTGC 10
DB 1 CDPXTGC 7
RESULT 8
ABJ00550
ID ABJ00550 standard; peptide; 7 AA.
XX
XX ABJ00550;
XX
XX 05-SEP-2002 (first entry)
XX
XX B lymphocyte stimulator protein binding peptide #1.
XX
XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
XX allergy; proliferative disease; infectious disease; arteriosclerosis;
XX inflammatory disorder; hypergammaglobulinaemia; blood clotting;
XX

KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritis;
KW neuroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;
KW antiaesthetic; antiallergic; thymimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX
XX FT Misc-difference 2 /label= Phe, Trp, Tyr
XX
XX FT Misc-difference 4 /label= Pro, Tyr
XX
XX
XX WO200216411-A2.
XX
XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US025850.
XX
XX 18-AUG-2000; 2000US-0226700P.
XX
XX (HUMA-) HUMA GENOME SCI INC.
XX
XX Belzer JP, Potter DM, Fleming TL, Rosen CA;
XX WPI; 2002-499775/53.
XX
XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX administering B lymphocyte stimulator binding polypeptide.
XX
XX Claim 69; Page 233; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
XX amelioration of a disease or disorder associated with: aberrant B
XX lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
XX of haematopoietic origin; or proliferative disease; and reducing
XX inhibiting or stimulating immunoglobulin production. B cell proliferation
XX and graft rejection involving administration of Blys binding polypeptide.
XX The Blys binding polypeptides are used in the treatment, prevention or
XX amelioration of diseases such as immune system diseases, proliferative
XX diseases, diseases of cells of haematopoietic origin, graft rejection,
XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX neurodegenerative diseases. The present sequence is a B lymphocyte
XX stimulator protein binding peptide
XX
XX Sequence 7 AA;
SQ
Query Match 77.3%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CXPXTGC 10
DB 1 CXPXTGC 7
RESULT 9
ABG33862
ID ABG33862 standard; peptide; 7 AA.
XX
XX ABG33862;
XX
XX 15-JUL-2002 (first entry)
XX
XX B lymphocyte stimulator (Blys) binding peptide #436.
XX
XX B lymphocyte stimulator protein; B lymphocyte stimulator binding peptide;
XX Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
XX synovial fluid; saliva; mucus.
XX

OS Synthetic.
 XX WO200216412-A2.
 PN
 XX
 XX 28-FEB-2002.
 PD
 XX 17-AUG-2001, 2001WO-US025891.
 XX PF
 XX 18-AUG-2000, 2000US-0226489P.
 XX
 XX (DYAX-) DYAX CORP.
 PA
 XX Beltez JP, Potter MD, Fleming TJ, Ladner RC;
 PI WPI, 2002-351647/38.
 XX
 XX New B-lymphocyte stimulator binding polypeptide useful in detecting or
 PT isolating Blys or Blys-like polypeptide comprises a specified amino acid
 PT sequence.
 XX
 XX Disclosure, Page 132; 269pp; English.
 PS
 XX The invention relates to a B lymphocyte stimulator (Blys) binding
 CC polypeptide. Blys binding peptides bind Blys or Blys-like proteins
 CC reversibly or irreversibly. The binding peptides are used in detection,
 CC isolation and/or purification of Blys in a solution such as water or a
 CC buffer solution, as well as any fluid and/or cell obtained from an
 CC individual biological fluid, body tissue, body cell, cell line, tissue
 CC culture or other source containing Blys or Blys-like polypeptides. The
 CC biological fluids include sera, plasma, lymph, and mucous. Sequences
 CC urine, synovial fluid, spinal fluid, saliva and mucous. Sequences
 CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
 CC ABG33852-33862 represent Blys binding peptides of the invention
 CC
 XX Sequence 7 AA;
 SQ
 Query Match 77.3%; Score 34; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 CXPXTGC 10
 Db 1 CXPXTGC 7
 XX
 XX RESULT 10
 ABJ00545
 ID ABJ00545 standard; peptide; 13 AA.
 XX
 AC ABJ00545;
 XX
 DT 05-SEP-2002 (first entry)
 XX
 DE B lymphocyte stimulator protein binding protein consensus peptide #1.
 XX
 XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
 KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
 KW antiaesthetic; anti-allergic; chytromelic; antianemic; haemostatic;
 KW dermatological; anti-inflammatory; cardiac; opthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.
 KW
 XX Undentified.
 OS
 XX Key Location/Qualifiers
 FH MISC-difference 1 /label= Ala, Asn, Lys, Ser
 FT MISC-difference 2 /label= Ala, Glu, Met, Ser, Val
 FT MISC-difference 3

FT /label= Ala, Asn, Lys, Pro
 FT MISC-difference 5 /label= Phe, Trp, Tyr
 FT MISC-difference 7
 FT MISC-difference 7 /label= Pro, Tyr
 FT MISC-difference 11
 FT MISC-difference 12 /label= Ala, Glu, His, Phe, Val
 FT MISC-difference 12 /label= Asn, Glu, Gly, His, Ser, Val
 FT MISC-difference 13 /label= Ala, Asn, Gly, Ile, Pro, Ser
 FT
 XX
 XX WO200216411-A2.
 PN
 XX 28-FEB-2002.
 PD
 XX 17-AUG-2001, 2001WO-US025850.
 XX PF
 XX 18-AUG-2000, 2000US-0226700P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Beltez JP, Potter DM, Fleming TJ, Rosen CA;
 XX WPI, 2002-499775/53.
 XX
 XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
 PT administering B lymphocyte stimulator binding polypeptide.
 PT
 XX Claim 69; Page 230; 387pp; English.
 PS
 XX The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of Blys binding polypeptide.
 CC The Blys binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of haematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a conserved region of
 CC a B lymphocyte stimulator protein binding peptide
 CC
 XX Sequence 13 AA;
 SQ
 Query Match 77.3%; Score 34; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 CXPXTGC 10
 Db 4 CXPXTGC 10
 XX
 XX RESULT 11
 ABG33861
 ID ABG33861 standard; peptide; 13 AA.
 XX
 AC ABG33861;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE B lymphocyte stimulator (Blys) binding peptide #435.
 XX
 XX B lymphocyte stimulator protein; B lymphocyte stimulator binding peptide;
 KW Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
 KW synovial fluid; saliva; mucus.
 KW
 XX Synthetic.
 OS
 XX WO200216412-A2.
 PN


```
XX 28-FEB-2002.
PD
XX 17-AUG-2001; 2001WO-US025891.
XX
XX 18-AUG-2000; 2000US-0226489P.
XX
XX (DYAX-) DYAX CORP.
XX
XX Beltzer JP, Potter MD, Fleming TJ, Ladner RC;
XX WPI; 2002-351647/38.
XX
XX New B-lymphocyte stimulator binding polypeptide useful in detecting or
XX isolating Bly8 or Bly8-like polypeptide comprises a specified amino acid
XX sequence.
XX
XX Disclosure; Page 121; 269pp; English.
XX
XX The invention relates to a B lymphocyte stimulator (Bly8) binding
XX polypeptide. Bly8 binding peptides bind Bly8 or Bly8-like proteins
XX reversibly or irreversibly. The binding peptides are used in detection,
XX isolation and/or purification of Bly8 in a solution such as water or a
XX buffer solution, as well as any fluid and/or cell obtained from an
XX individual biological fluid, body tissue, body cell, cell line, tissue
XX culture or other source containing Bly8 or Bly8-like polypeptides. The
XX biological fluids include sera, plasma, lymph, blood, blood fraction,
XX urine, synovial fluid, spinal fluid, saliva and mucous. Sequences
XX ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
XX ABG33852-33862 represent Bly8 binding peptides of the invention
XX
XX
XX Sequence 13 AA;
SQ
XX
XX Query Match 77.3%; Score 34; DB 5; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 19;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CXPXTGC 10
DB 4 CXPXTGC 10
XX
XX RESULT 12
XX AAU44932
XX ID AAU44932 standard; protein; 53 AA.
XX
XX AAU44932;
XX
XX 27-FEB-2002 (first entry)
XX
XX Propionibacterium acnes immunogenic protein #5828.
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX dermatological; osteopathic; neuroprotectant.
XX
XX Propionibacterium acnes.
XX
XX WO200181581-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US012865.
XX
XX 21-APR-2000; 2000US-0199047P.
XX 02-JUN-2000; 2000US-0208841P.
XX 07-JUL-2000; 2000US-0216747P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX L'maisonneuve J, Zhang Y, Jen S, Carter D;
```

```
XX WPI; 2001-616774/71.
XX
XX N-PSDB; AAS59524.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
XX PT vaccinating against and diagnosing infections, especially useful for
XX PT treating acne vulgaris.
XX
XX Example 1; SEQ ID NO 6127; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
XX polypeptides. The proteins and their associated DNA sequences are used in
XX the treatment, prevention and diagnosis of medical conditions caused by
XX P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
XX pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
XX P. acnes is also involved in infections of bone, joints and the central
XX nervous system, however it is particularly involved in the inflammatory
XX lesions associated with acne vulgaris. A method for detecting the
XX presence or absence of P. acnes in a patient comprises contacting a
XX sample with a binding agent that binds to the proteins of the invention
XX and determining the amount of bound protein in the sample. The
XX polypeptides may be used as antigens in the production of antibodies
XX specific for P. acnes proteins. These antibodies can be used to
XX downregulate expression and activity of P. acnes polypeptides and
XX therefore treat P. acnes infections. The antibodies may also be used as
XX diagnostic agents for determining P. acnes presence, for example, by
XX enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX
XX Sequence 53 AA;
SQ
XX
XX Query Match 77.3%; Score 34; DB 4; Length 53;
XX Best Local Similarity 71.4%; Pred. No. 60;
XX Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CXPXTGC 10
DB 33 CRPRTGC 39
XX
XX RESULT 13
XX ABM41451
XX ID ABM41451 standard; protein; 53 AA.
XX
XX ABM41451;
XX
XX 20-OCT-2003 (first entry)
XX
XX Propionibacterium acnes predicted ORF-encoded polypeptide #6127.
XX
XX Acne vulgaris; antiheborrhoeic; dermatological; antibacterial;
XX immunostimulant; immune response; vaccine.
XX
XX Propionibacterium acnes.
XX
XX WO2003033515-A1.
XX
XX 24-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032727.
XX
XX 15-OCT-2001; 2001US-00978825.
XX
XX (CORI-) CORIXA CORP.
XX
XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
XX Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
XX Barth B, Valliave-Douglas J;
XX
XX WPI; 2003-381789/36.
XX N-PSDB; ACP64453.
```

XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PI or for stimulating an immune response specific for a P. acnes protein.
XX

PS Example 1, SEQ ID NO 6127, 1481bp, English.

XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention; antibodies against polypeptides of the
CC invention; fusion proteins comprising a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising P. acnes polypeptides,
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX

SO Sequence 53 AA:

Query Match 77.3%; Score 34; DB 6; Length 53;
Best Local Similarity 71.4%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CXPXTGC 10
Db 33 CRPRTGC 39

RESULT 14

ID ADA54961 standard; protein; 113 AA.

XX ADA54961;

XX 20-NOV-2003 (first entry)

XX Human protein, SEQ ID 2529.

XX Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KM Gene Therapy; human; secretory protein; membrane proteins; cancer;
KM inflammatory disease; osteoporosis; neurological disease.

XX Homo sapiens.

OS EPI293569-A2.

XX EPI293569-A2.

XX 19-MAR-2003.

XX 21-MAR-2002; 2002EP-0000586.

XX 14-SEP-2001; 2001JP-00328381.

XX 24-JAN-2002; 2002US-0350435P.
XX (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y,
XX

DR WPI; 2003-395539/38.
XX N-PSDB; ADA53322.

XX New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PT which the gene is involved, or as target molecules for gene therapy.

PS Claim 14; SEQ ID NO 2529; 205bp; English.

XX The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
CC inflammatory diseases, osteoporosis or neurological disease.

XX Sequence 113 AA:

Query Match 77.3%; Score 34; DB 6; Length 113;
Best Local Similarity 71.4%; Pred. No. 1,1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CXPXTGC 10
Db 103 CXPXTGC 109

RESULT 15

ID AAB42027 standard; protein; 138 AA.

XX AAB42027;

XX 08-FEB-2001 (first entry)

XX Human ORFX ORF1791 polypeptide sequence SEQ ID NO:3582.

XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KM vulnerary; antiparasitic; antiparkinsonian; nootropic; neuroprotective;
KM anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KM immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KM hypotensive; dermatological; immunosuppressive; antiinflammatory;
KM antiviral; antibacterial; antifungal; antirheumatic; antitumor;
KM antianemic; gene therapy; cancer; proliferative disorder; hypertension;
KM neurodegenerative disorder; osteoarthritis; graft vs host disease;
KM cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KM cholesterol ester storage; systemic lupus erythematosus; infection;
KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KM bone damage; cartilage damage; antiinflammatory disease; coagulation;
KM thrombosis; contraceptive.

XX Homo sapiens.

XX WO200058473-A2.

XX 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US008621.

XX 31-MAR-1999; 99US-0127607P.

XX 02-APR-1999; 99US-0127636P.

XX 05-APR-1999; 99US-0127728P.

XX 30-MAR-2000; 2000US-00540763.

XX (CURA-) CURAGEN CORP.
XX Shinketsu RA, Leach M,
PI

DR WPI; 2000-602362/57.
DR N-PsDB; AAC76236.

PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease.

PS Claim 11; Page 2743; 5507pp; English.

XX AAC74446 to AAC7606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
CC antiproliferative; antiparkinsonian; nootropic; neuroprotective; osteopathic;
CC anticonvulsant; antiallergic; immunosuppressant; immunostimulant;
CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
CC antiviral; antifungal; antitumoric; antithyroid; and antianaemic. The
CC sequences can be used for determining the presence of or predisposition
CC to, or preventing or treating pathological conditions associated with an
CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC proteins in gene therapy vectors. The proteins and nucleic acids may be
CC used to treat cancers, proliferative disorders, neurodegenerative
CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC storage, systemic lupus erythematosus, severe combined immunodeficiency
CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
CC enhance coagulation; to inhibit thrombosis; and as a contraceptive

XX Sequence 138 AA;

Query Match 77.3%; Score 34; DB 3; Length 138;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CXPXTGC 10
DB 15 CGPRTGC 21

Search completed: January 12, 2005, 23:10:52
Job time : 150.9 secs

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OW protein - protein search, using sw model

Run on: January 12, 2005, 23:04:08 ; Search time 16.8 seconds
(without alignments)

40.090 Million cell updates/sec

Title: US-09-932-322-8

Perfect score: 38

Sequence: 1 CXPXTGC 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	94.7	601	2	A27020
2	34	89.5	145	2	S07983
3	34	89.5	312	2	T05348
4	33	86.8	1058	2	T50496
5	32	84.2	64	2	F96006
6	31	81.6	482	2	T48397
7	31	81.6	643	2	T25473
8	30	78.9	132	2	A24255
9	30	78.9	129	2	B24255
10	30	78.9	151	2	AB0331
11	30	78.9	199	2	T49486
12	30	78.9	200	2	S04926
13	30	78.9	201	2	T07729
14	30	78.9	211	2	T04098
15	30	78.9	221	1	S04927
16	30	78.9	222	1	MMVZB4
17	30	78.9	224	2	E84326
18	30	78.9	336	2	AB3801
19	30	78.9	345	1	MMVZM2
20	30	78.9	406	2	T23898
21	30	78.9	430	2	T23899
22	30	78.9	551	2	S01793
23	30	78.9	551	2	S07089
24	30	78.9	648	2	T23864
25	30	78.9	1722	2	H8753
26	29	76.3	46	2	H71262
27	29	76.3	119	2	B45937
28	29	76.3	119	2	S24292
29	29	76.3	119	2	S24292
29	29	76.3	119	2	S24294

30	29	76.3	119	2	S24291	chorion protein -
31	29	76.3	121	2	S24293	chorion class CA p
32	29	76.3	147	2	E82523	hypothetical prote
33	29	76.3	163	2	T33130	hypothetical prote
34	29	76.3	245	2	F84680	hypothetical prote
35	29	76.3	333	2	F90172	hypothetical prote
36	29	76.3	348	2	T35248	probable oxidoredu
37	29	76.3	375	2	A83636	hypothetical prote
38	29	76.3	379	2	S14885	hypothetical prote
39	29	76.3	449	2	E96676	hypothetical prote
40	29	76.3	507	2	T23375	hypothetical prote
41	29	76.3	513	2	D88991	protein apx-1 (imp
42	29	76.3	685	2	UC7570	Delta-4 protein -
43	29	76.3	686	2	UC7569	Delta-4 protein -
44	29	76.3	753	2	T28787	hypothetical prote
45	29	76.3	843	1	A27340	complement C7 prec

ALIGNMENTS

RESULT 1
A27020
DIF-induced prestalk pdd63 protein precursor - slime mold (Dictyostelium discoideum) (E
C/Species: Dictyostelium discoideum
C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C/Accession: A27020
R/Williams, J.G.; Caccarelli, A.; McRobbie, S.; Mahubani, H.; Kay, R.R.; Early, A.; Be
Cell 49, 185-192, 1987
A/Title: Direct induction of Dictyostelium prestalk gene expression by DIF provides evi
A/Reference number: A27020; MUID:87187613; PMID:3568124
A/Accession: A27020
A/Molecule type: DNA
A/Residues: 1-601 <MT>
A/Cross-references: UNIPROT:Q7M4U3
C/Genetic8:
A/Genes: pdd63
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-601/Product: DIF-induced prestalk pdd63 protein #status predicted <MAT>

Query Match 94.7%; Score 36; DB 2; Length 601;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXPXTGC 7
DB 245 CXPXTGC 251

RESULT 2
S07983
phospholipase A2 homolog precursor - common tiger snake
C/Species: Notechis scutatus scutatus (common tiger snake, mainland tiger snake)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C/Accession: S07983
R/Puancel, F.
Submitted to the EMBL Data Library, January 1989
A/Reference number: S07983
A/Accession: S07983
A/Molecule type: mRNA
A/Residues: 1-145 <DUC>
A/Cross-references: UNIPROT:P20146; EMBL:X14043; NID:G64109; PIDN:CAA32201.1; PID:G6411
F/1-27/Domain: signal sequence #status predicted <SIG>
F/28-145/Product: phospholipase A2 #status predicted <MAT>

Query Match 89.5%; Score 34; DB 2; Length 145;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXPXTGC 7
DB 105 CXPXTGC 111

RESULT 3
 T05348
 hypothetical protein FB84.80 - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C/Accession: T05348
 R/Bevan, M.; Terry, N.; Ardiles, W.; Buyssebaert, C.; Daseville, R.; De Clerck, R.; De ewes, H.W.; Meyer, K.F.X.; Scheller, C.
 submitted to the Protein Sequence Database, February 1999
 A/Reference number: 215409
 A/Accession: T05348
 A/Molecule type: DNA
 A/Residues: 1-312 <BEV>
 A/Cross-references: UNIPROT:Q98UV3; EMBL:AL034567
 A/Experimental source: cultivar Columbia; BAC clone FB84
 C/Genetics:
 A/Map position: 4
 A/Intons: 1/3; 44/3; 101/3; 139/3; 180/3
 A/Note: FB84.80

Query Match 89.5%; Score 34; DB 2; Length 312;
 Best Local Similarity 71.4%; Pred. No. 32;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CXPXTGC 7
 DB 208 CDPPTGC 214

RESULT 4
 T50496
 hypothetical protein T22D6.50 - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
 C/Accession: T50496
 R/Bevan, M.; Terry, N.; Ardiles, W.; Buyssebaert, C.; Daseville, R.; De ewes, H.W.; Rudd, S.; Lemcke, K.; Meyer, K.F.X.
 submitted to the Protein Sequence Database, May 2000
 A/Reference number: 225101
 A/Accession: T50496
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-1058 <BEV>
 A/Cross-references: UNIPROT:Q9LEZ5; EMBL:AL357612
 A/Experimental source: cultivar Columbia; BAC clone T22D6
 C/Genetics:
 A/Map position: 5
 A/Intons: 60/3; 195/3; 222/3; 448/3; 492/3; 526/3; 555/2; 591/2; 616/3; 662/2; 715/3; 7
 A/Note: T22D6.50

Query Match 86.8%; Score 33; DB 2; Length 1058;
 Best Local Similarity 71.4%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CXPXTGC 7
 DB 1019 CDPPTGC 1025

RESULT 5
 F96006
 hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSymB
 C/Species: Sinorhizobium meliloti
 C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C/Accession: F96006
 R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A/Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo A/Reference number: A95842; MUID:21396508; PMID:11481431
 A/Accession: F96006
 A/Status: preliminary

A/Molecule type: DNA
 A/Residues: 1-64 <KUR>
 A/Cross-references: UNIPROT:Q92U25; GB:AL591985; PIDN:CAC49718.1; PID:G15141205; GSPDB: R/Galbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abolia, P.; Barloy-Hubler pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F. L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure hebut, P.; Vandenhol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yen, K A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A/Reference number: A96039; MUID:21368234; PMID:11474104
 A/Contents: annotation
 C/Genetics:
 A/Genes: SMD21688
 A/Genome: plasmid

Query Match 84.2%; Score 32; DB 2; Length 64;
 Best Local Similarity 57.1%; Pred. No. 22;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CXPXTGC 7
 DB 15 CAPSSGC 21

RESULT 6
 T48397
 S-receptor kinase-like protein - Arabidopsis thaliana
 N/Alternate names: protein P17C15.120
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C/Accession: T48397
 R/Bevan, M.; Pohl, T.; Welzenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.
 submitted to the Protein Sequence Database, March 2000
 A/Reference number: 224492
 A/Accession: T48397
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-482 <BEV>
 A/Cross-references: UNIPROT:Q9LZB8; EMBL:AL162506
 A/Experimental source: cultivar Columbia; BAC clone P17C15
 C/Genetics:
 A/Map position: 5
 A/Note: P17C15.120

Query Match 81.6%; Score 31; DB 2; Length 482;
 Best Local Similarity 57.1%; Pred. No. 1.6e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CXPXTGC 7
 DB 301 CTPSGC 307

RESULT 7
 T23473
 hypothetical protein B0507.1 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T23473
 R/Bradehaw, H.
 submitted to the EMBL Data Library, July 1996
 A/Description: The sequence of C. elegans cosmid B0507.
 A/Reference number: Z20039
 A/Accession: T23473
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-643

 A/Cross-references: UNIPROT:Q22886; EMBL:U64833; PIDN:AA04882.1; GSPDB:GN00023; CESP:B A/Experimental source: strain Bristol N2; clone B0507
 C/Genetics:
 A/Genes: CESP:B0507.1

A/Map position: 5
A/Introns: 59/3; 133/1; 464/3; 586/1

Query Match
Best Local Similarity 81.6%; Score 31; DB 2; Length 643;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CKPXTGC 7
DB 209 CEFQSGC 215

RESULT 8

A24255
Chorion class A protein L11 precursor - silkworm
C/Species: Bombyx mori (silkworm)
C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C/Accession: A24255
R/Spoerel, N.; Nguyen, H.T.; Kafatos, F.C.
J. Mol. Biol. 190, 23-35, 1986

A/Title: Gene regulation and evolution in the chorion locus of Bombyx mori. Structural
A/Reference number: A92929; PMID:87060979; PMID:3023635

A/Accession: A24255
A/Molecule type: DNA
A/Residues: 1-129 <SPO>

A/Cross-references: UNIPROT:P08826; GB:X15557; GB:X04028; GB:X04029; GB:X04030; GB:X04031

C/Species: Chorion class A protein pc292
C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C/Accession: F12-129/Domain: signal sequence #status predicted <SIG>

F12-129/Product: chorion class A protein L11 #status predicted <MAT>

Query Match
Best Local Similarity 78.9%; Score 30; DB 2; Length 129;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CKPXTGC 7
DB 116 CAPTGC 122

RESULT 9

B24255
Chorion class A protein L12 precursor - silkworm

C/Species: Bombyx mori (silkworm)
C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C/Accession: B24255
R/Spoerel, N.; Nguyen, H.T.; Kafatos, F.C.
J. Mol. Biol. 190, 23-35, 1986

A/Title: Gene regulation and evolution in the chorion locus of Bombyx mori. Structural
A/Reference number: A92929; PMID:87060979; PMID:3023635

A/Accession: B24255
A/Molecule type: DNA
A/Residues: 1-132 <SPO>

A/Cross-references: UNIPROT:P08825; GB:X15557; GB:X04028; GB:X04029; GB:X04030; GB:X04031

C/Species: Chorion class A protein pc292
C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C/Accession: F12-132/Domain: signal sequence #status predicted <SIG>

F12-132/Product: chorion class A protein L12 #status predicted <MAT>

Query Match
Best Local Similarity 78.9%; Score 30; DB 2; Length 132;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CKPXTGC 7
DB 117 CAPTGC 123

RESULT 10

AB0331
sigma E factor regulatory protein rsec [imported] - Yersinia pestis (strain CO92)

C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C/Accession: AB0331
R/Perkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001

A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; PMID:21470413; PMID:11586360

A/Accession: AB0331
A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-151 <NUR>
A/Cross-references: UNIPROT:Q8ZD76; GB:AL590842; PIDN:CMC92953.1; PID:G15980692; GSPDB:
C/Genetics: rsec

A/Genetic: rsec
C/Superfamily: Escherichia coli sigma-E factor regulatory protein rsec

Query Match
Best Local Similarity 78.9%; Score 30; DB 2; Length 151;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CKPXTGC 7
DB 20 CEPHSGC 26

RESULT 11

T49486
hypothetical protein B14D6.380 [imported] - Neurospora crassa

C/Species: Neurospora crassa
C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C/Accession: T49486
R/Schulte, U.; Algen, V.; Hohenstein, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura

submitted to the Protein Sequence Database, May 2000
A/Reference number: Z25022

A/Status: preliminary
A/Accession: T49486
A/Molecule type: DNA

A/Residues: 1-199 <SCH>
A/Cross-references: EMBL:AL556173; GSPDB:GN00116; NCSP:B14D6.380

A/Experimental source: BAC clone B14D6; strain OR74A.
C/Genetics:
A/Genetic: NCSP:B14D6.380

A/Map position: 6
C/Superfamily: Neurospora crassa hypothetical protein B14D6.380

Query Match
Best Local Similarity 78.9%; Score 30; DB 2; Length 199;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CKPXTGC 7
DB 155 CKPLSGC 161

RESULT 12

S04926
wound-induced protein 1 precursor - potato

C/Species: Solanum tuberosum (potato)
C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C/Accession: S04926
R/Stamford, A.; Bevan, M.; Northcote, D.

Mol. Gen. Genet. 215, 200-208, 1989
A/Title: Differential expression within a family of novel wound-induced genes in potato

A/Reference number: S04926; PMID:89218921; PMID:2710099

A/Accession: S04926
A/Molecule type: DNA

A/Residues: 1-200 <STA>
A/Cross-references: UNIPROT:P09761; EMBL:X13497; NID:G21617; PIDN:CAA31851.1; PID:G2161

C/Genetics:
A/Genetic: win1

A/Introns: 143/3
C/Superfamily: hevein precursor; barvin homology; hevein chitin-binding domain homology

F12-25/Domain: signal sequence #status predicted <SIG>
F12-25/Product: wound-induced protein 1 #status predicted <MAT>

F12-25/Domain: hevein chitin-binding domain homology <HCB>

F/78-199/Domain: barwin homology <BAR>

Query Match 78.9%; Score 30; DB 2; Length 200;
Best Local Similarity 57.1%; Pred. NO. 1.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CXPTGTC 7
DB 56 CSPSGGC 62

RESULT 13

T07729

Wound-induced protein (clone TAB7) - tomato (fragment)

C/Species: Lycopersicon esculentum (tomato)

C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004

C/Accession: T07729

R/Harris, N.; Taylor, J.E.; Roberts, J.A.

J. Exp. Bot. 48, 1231-1227, 1997

A/Title: Characterization and expression of an mRNA encoding a wound-induced (win) prote

A/Reference number: 216099

A/Accession: T07729

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-201 <HAR>

A/Cross-references: UNIPROT:O03994; EMBL:U89764; NID:G1888560; PIDN:AB49688.1; PID:G188

A/Experimental source: strain A15a craf; leaf abscission zone tissue

C/Superfamily: hevein precursor; barwin homology; hevein chitin-binding domain homology

F/16-66/Domain: hevein chitin-binding domain homology <HCB>

F/68-188/Domain: barwin homology <BAR>

Query Match 78.9%; Score 30; DB 2; Length 201;
Best Local Similarity 57.1%; Pred. NO. 1.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CXPTGTC 7
DB 46 CSPSGGC 52

RESULT 14

T04098

CBP20 preproprotein - common tobacco

N/Alternate names: wound-induced protein

C/Species: Nicotiana tabacum (common tobacco)

C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C/Accession: T04098

R/Bonsstein, A.S.; Bress-Vioemann, S.A.; Sela-Buurlage, M.B.; Elzen, P.J.; Melchere, L.S.;

Plant Physiol. 104, 109-118, 1994

A/Title: A novel pathogen- and wound-inducible tobacco (Nicotiana tabacum) protein with

A/Reference number: 215209; MUID:94159785; PMID:8115541

A/Accession: T04098

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-211 <PON>

A/Cross-references: UNIPROT:Q41231; EMBL:S72452; NID:G632733; PIDN:AB29959.1; PID:G6327

A/Experimental source: cultivar Samum NN

C/Superfamily: hevein precursor; barwin homology; hevein chitin-binding domain homology

F/23-66/Domain: hevein chitin-binding domain homology <HCB>

F/78-199/Domain: barwin homology <BAR>

Query Match 78.9%; Score 30; DB 2; Length 211;
Best Local Similarity 57.1%; Pred. NO. 1.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CXPTGTC 7
DB 53 CSPSGGC 59

RESULT 15

S04927

wound-induced protein 2 precursor - potato

C/Species: Solanum tuberosum (potato)

C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004

C/Accession: S04927

R/Stamford, A.; Bevan, M.; Northcote, D.

Mol. Gen. Genet. 215, 200-208, 1989

A/Title: Differential expression within a family of novel wound-induced genes in potato

A/Reference number: S04926; MUID:89218921; PMID:2710099

A/Accession: S04927

A/Molecule type: DNA

A/Residues: 1-211 <STA>

A/Cross-references: UNIPROT:P09762; EMBL:X13497; NID:G21617; PIDN:CAA31852.1; PID:G2161

C/Genetics:

A/Gene: win2

A/Intons: 142/3

C/Superfamily: hevein precursor; barwin homology; hevein chitin-binding domain homology

F/1-25/Domain: signal sequence #status predicted <SIG>

F/26-211/Product: wound-induced protein 2 #status predicted <MAT>

F/77-198/Domain: hevein chitin-binding domain homology <HCB>

Query Match 78.9%; Score 30; DB 2; Length 211;
Best Local Similarity 57.1%; Pred. NO. 1.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CXPTGTC 7
DB 56 CSPSGGC 62

Search completed: January 12, 2005, 23:16:03
Job time: 16.8 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2005, 22:56:08 ; Search time 88.55 Seconds
(without alignment)
45.484 Million cell updates/sec

Title: US-09-932-322-8
Perfect score: 38
Sequence: 1 CXPXTC 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : uniprot_02:*
1: uniprot_prot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	94.7	192	098AR9	098AR9 rhizobium 1
2	36	94.7	350	086AK7	086AK7 dictyostelium 1
3	36	94.7	546	08KJ72	08KJ72 rhizobium 1
4	36	94.7	601	07M4J3	07M4J3 dictyostelium 1
5	35	92.1	148	09N018	09N018 macaca fasc
6	35	92.1	148	09SKD2	09SKD2 macaca fasc
7	35	92.1	571	09AQP5	09AQP5 pseudomonas
8	34	89.5	113	07Z6C7	07Z6C7 homo sapien
9	34	89.5	145	PA2X_NOTSC	P2016 notechia bc
10	34	89.5	167	07U7V9	07U7V9 synchococc
11	34	89.5	312	09STV3	09STV3 arbidopsis
12	34	89.5	465	06TVH9	06TVH9 bovine papu
13	34	89.5	465	AA898366	AA898366 bovine pa
14	34	89.5	574	08LJ36	08LJ36 oryza sativ
15	34	89.5	998	0869K4	0869K4 dictyostelium 1
16	34	89.5	2217	0869K4	0869K4 dictyostelium 1
17	34	89.5	2217	0869K4	0869K4 dictyostelium 1
18	34	89.5	2217	0869K4	0869K4 dictyostelium 1
19	33	86.8	464	07XV21	07XV21 oryza sativ
20	33	86.8	1058	09LZS5	09LZS5 arbidopsis
21	33	86.8	1468	080TF6	080TF6 mus musculi
22	32	84.2	64	092J25	092J25 rhizobium m
23	32	84.2	123	0926M4	0926M4 listeria in
24	32	84.2	520	06Z8K1	06Z8K1 oryza sativ
25	32	84.2	520	BAD15642	BAD15642 oryza sat
26	32	84.2	1152	09FI26	09FI26 arbidopsis
27	31	81.6	162	09WU17	09WU17 mesocricetu
28	31	81.6	166	08T415	08T415 mesocricetu
29	31	81.6	239	093KV9	093KV9 streptomyce
30	31	81.6	342	06VW44	06VW44 streptomyce
31	31	81.6	342	AA830165	AA830165 streptomyce
32	31	81.6	361	08ECT9	08ECT9 shewanella

32	31	81.6	482	2	09LZR8	09LZR8 arbidopsis
33	31	81.6	615	2	022886	022886 caenorhabdi
34	30	78.9	66	2	07N375	07N375 photorhabdu
35	30	78.9	78	2	P90569	P90569 plasmidium
36	30	78.9	95	2	P77130	P77130 escherichia
37	30	78.9	100	1	CHA3_BOMMO	CHA3_BOMMO bombyx mori
38	30	78.9	114	2	08M078	08M078 caenorhabdi
39	30	78.9	119	2	08P958	08P958 xanthomonas
40	30	78.9	129	1	CHA1_BOMMO	CHA1_BOMMO bombyx mori
41	30	78.9	132	1	09LIW4	09LIW4 oryza sativ
42	30	78.9	133	2	06D216	06D216 erwinia car
43	30	78.9	150	2	08ZD76	08ZD76 yersinia pe
44	30	78.9	151	2	AA62716	AA62716 yersinia pe
45	30	78.9	151	2	AA62716	AA62716 yersinia pe

ALIGNMENTS

RESULT 1

ID 098AR9 PRELIMINARY; PRT; 192 AA.
AC 098AR9;
DT 01-OCT-2001 (Tremblrel. 18, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE M15880 protein.
GN OrderedlocusNames=M15880;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAF303099;
RC MEDLINE=21082930; PubMed=11214974;
RA Kaneo T., Nakamura Y., Sato S., Aeamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idekawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsuno M.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.,
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti (supplement).";
RL DNA Res. 7:381-406(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MAF303099;
RC MEDLINE=21082930; PubMed=11214968;
RA Kaneo T., Nakamura Y., Sato S., Aeamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idekawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsuno M.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.,
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-336(2000).
DR EMBL: AP003007; BAB52253.1; --
DR HSSP: Q9ZFY9; 1FK8
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR002198; ADH_short.
DR InterPro: IPR002347; ADH_short_C2.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00081; GDBRDH.
KW Complete proteome.
SQ SQUENCB 192 AA; 20183 MW; PD28660D156037BC CRC64;

Query Match 94.7%; Score 36; DB 2; Length 192;
Best Local Similarity 71.4%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Ox 1 CXPXTC 7

Db 176 CSPATGC 182

RESULT 2

Q86AK7 PRELIMINARY; PRT; 360 AA.
 AC Q86AK7;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Similar to Dictyostelium discoideum (Slime mold). Prestalk protein.
 OS Dictyostelium discoideum (Slime mold).
 CC Eukaryota; Mycetozoa; Dictyostelid; Dictyostelium.
 NCBI_TaxId=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RX MEDLINE=22092622; PubMed=12097910;
 RA Gloeckner G., Richinger L., Szafrański K., Pachecat J., Dear P., Lohmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tüngel B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
 RT [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA Baumgart C.;
 RL Submitted (MAR-2003) to the EMBL/Genbank/DBJ databases.
 DR HSBP; P01382; INTN.
 DR InterPro; IPR002172; LDL_receptor_A.
 DR InterPro; IPR001673; S_mold_repeat.
 DR Pfam; PF00526; Dicy_CTDG; 13.
 DR PRINTS; PR00261; LDLRECEPTOR.
 SQ SEQUENCE 360 AA; 38013 MW; 480061AB26ED81E CRC64;

Query Match 94.7%; Score 36; DB 2; Length 360;
 Best Local Similarity 71.4%; Pred. No. 49;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXPXTC 7
 Db 211 CSPSTGC 217

RESULT 3

Q8KJ72 PRELIMINARY; PRT; 546 AA.
 AC Q8KJ72;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE PUTATIVE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE PROTEIN.
 GN Name=mg1329;
 OS Rhizobium loti (Mesorhizobium loti).
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 NCBI_TaxId=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R7A;
 RX MEDLINE=21992722; PubMed=12003951;
 RA Sullivan J.T., Trzebiatowski J.R., Cnicksbank R.W., Gouzy J., Brown S.D., Elliott R.M., Fleetwood D.J., McCallum N.G., Rossbach U., Stuart G.S., Weaver J.B., Webb R.J., de Bruijn F.J., Ransom C.W.; "Comparative sequence analysis of the symbiosis island of Mesorhizobium loti strain R7A."; J. Bacteriol. 184:3086-3095(2002).
 RT [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Cerebellum cortex;
 RA Suzuki Y., Sugano S., Hashimoto K.;
 DR EMBL; AL672114; CAD31361.1; -.
 DR HSBP; P50163; ZARI.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR002198; ADH_short.

DR InterPro; IPR002347; Adh_short_C2.

DR Pfam; PF00106; adh_short; 2.

DR PRINTS; PRO0081; GDHRH.

DR PRINTS; PRO0080; SDRFAMILY.

DR PROSITE; PS00061; ADH_SHORT; 1.

KW Oxidoreductase.

SQ SEQUENCE 546 AA; 56900 MW; 091D2EFD8B55A9C CRC64;

Query Match 94.7%; Score 36; DB 2; Length 546;
 Best Local Similarity 71.4%; Pred. No. 72;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXPXTC 7
 Db 530 CSPATGC 536

RESULT 4

Q7MAJ3 PRELIMINARY; PRT; 601 AA.
 AC Q7MAJ3;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE DIF-induced prestalk pdd63 protein precursor (Fragments).
 OS Dictyostelium discoideum (Slime mold).
 CC Eukaryota; Mycetozoa; Dictyostelid; Dictyostelium.
 NCBI_TaxId=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87187613; PubMed=3568124;
 RA Williams J.G., Ceccarelli A., McRobbie S., Mahubani H., Kay R.R., Early A., Berks M., Jeremy K.A.; "Direct induction of Dictyostelium prestalk gene expression by DIF provides evidence that DIF is a morphogen."; Cell 49:185-192(1987).
 RT [1]
 RN Cell 49:185-192(1987).
 RL Cell 49:185-192(1987).
 DR PIR; A27020; A27020.
 DR InterPro; IPR001673; S_mold_repeat.
 DR Pfam; PF00526; Dicy_CTDG; 13.
 FT NON TER 601
 SQ SEQUENCE 601 AA; 63359 MW; 7D4433616CDAC438 CRC64;

Query Match 94.7%; Score 36; DB 2; Length 601;
 Best Local Similarity 71.4%; Pred. No. 79;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXPXTC 7
 Db 245 CSPSTGC 251

RESULT 5

Q9N018 PRELIMINARY; PRT; 148 AA.
 AC Q9N018;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Macaca fascicularis (Crested tit monkey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecinae; Macaca.
 NCBI_TaxId=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cerebellum cortex;
 RA Suzuki Y., Sugano S., Hashimoto K.;
 DR Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL; AB046629; BAB03547.1; -.
 KW Hypothetical protein.
 60 SEQUENCE 148 AA; 15495 MW; 62428CB430C6E13B CRC64;
 Query Match 92.1%; Score 35; DB 2; Length 148;
 Best Local Similarity 71.4%; Pred. No. 33;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CXPXTGC 7
 DB 74 CGPSTGC 80
 RESULT 6
 ID 095KD2 PRELIMINARY; PRT; 148 AA.
 AC 095KD2;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Macaca fascicularis (Crah eating macaque) (Cynomolpus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OC NCBI_TaxID=9541;
 RN [1]
 RP TISSUE=Medulla oblongata;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RA Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB062948; BAB60737.1; -.
 KW Hypothetical protein.
 60 SEQUENCE 148 AA; 15473 MW; C8D2A301E0C8191 CRC64;
 Query Match 92.1%; Score 35; DB 2; Length 148;
 Best Local Similarity 71.4%; Pred. No. 33;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CXPXTGC 7
 DB 74 CGPSTGC 80
 RESULT 7
 ID 09AQP5 PRELIMINARY; PRT; 571 AA.
 AC 09AQP5;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Putative ABC transporter subunit.
 GN Name=ORF31;
 OS Pseudomonas resinovorans.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OC NCBI_TaxID=53412;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CA10;
 RA MEDLINE=97386424; PubMed=9244273;
 RA Sato S., Ouchiyaama N., Kimura T., Nojiri H., Yamane H., Omori T.;
 RA "Cloning of genes involved in carbazole degradation of Pseudomonas sp.
 RT strain CA10: nucleotide sequence of genes and characterization of
 RT meta-clavage enzymes and hydrolyase.";
 RL J. Bacteriol. 179:4841-4849(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CA10;
 RA MEDLINE=97386425; PubMed=9244274;
 RA Sato S., Nam J., Kasuga K., Nojiri H., Yamane H., Omori T.;
 RA "Identification and characterization of genes encoding carbazole 1,9a-

RT dioxigenase in Pseudomonas sp. strain CA10.";
 RL J. Bacteriol. 179:4850-4858(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CA10;
 RA MEDLINE=21264379; PubMed=11371531;
 RA Nojiri H., Sekiguchi H., Maeda K., Urata M., Nakai S., Yoshida T.,
 RA Habe H., Omori T.;
 RA "Genetic characterization and evolutionary implications of car gene
 RT cluster in carbazole-degrader, Pseudomonas sp. strain CA10.";
 RL J. Bacteriol. 183:3663-3679(2001).
 DR EMBL; AB047548; BAB32742.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001851; Bac_inmem_transp.
 DR InterPro; IPR001865; Ribosomal_S2.
 DR Pfam; PF02653; BPD_transp_2; 2.
 DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
 SQ SEQUENCE 571 AA; 60653 MW; 9A685477078C186 CRC64;
 Query Match 92.1%; Score 35; DB 2; Length 571;
 Best Local Similarity 71.4%; Pred. No. 12e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CXPXTGC 7
 DB 565 CGPSTGC 571
 RESULT 8
 ID 07Z6J7 PRELIMINARY; PRT; 113 AA.
 AC 07Z6J7;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Krzywicki M.I., Skalska J., Smallos D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=lung;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC053646; AAH53646.1; -.
 KW Hypothetical protein.

80 SEQUENCE 113 AA; 11613 MW; 8624A42297FA43FF CRC64;
 Query Match 89.5%; Score 34; DB 2; Length 113;
 Best Local Similarity 71.4%; Pred. No. 40;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CXPXTC 7
 Db 103 CYPXTC 109

RESULT 9
 PA2X NOTSC STANDARD; PRT; 145 AA.
 ID PA2X NOTSC
 AC P2016;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DB Probable phospholipase A2 precursor (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase).
 OS Norechis scutatus scutatus (Mainland tiger snake) (Common tiger snake).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroides;
 OC Elapidae; Acanthophiinae; Norechis.
 OX NCBI_TaxID=70142;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISUVE-Venom gland;
 RA Duncanson F.;
 RL Submitted (JAN-1989) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acylglycerol groups in 3-sn-phosphoglycerides.
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerol + phosphocholine + a carboxylate.
 CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the phospholipase A2 family. Group I subfamily.

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 CC -----
 DR EMBL; X14043; CAA32201.1; -
 DR PIR; S07983; S07983.
 DR HSBP; P00608; 1A27.
 DR InterPro; IPR001211; PhospholipaseA2.
 DR Pfam; PF00068; PhospholipaseA2.1.
 DR PRINTS; PR00389; PHPLIPASEA2.
 DR PRODOM; PD00303; PhospholipaseA2.1.
 DR SMART; SM00085; PA2c; 1.
 DR PROSITE; PS00119; PA2_ASP; 1.
 DR PROSITE; PS00118; PA2_HIS; 1.
 KW Calcium; Hydrolase; Lipid degradation; Multigene family; Signal.
 FT SIGNAL 1 21
 FT PROPE 22 27
 FT CHAIN 28 145
 FT ACT_SITE 25 75
 FT ACT_SITE 119 119
 FT DISULFID 38 98
 FT DISULFID 54 144
 FT DISULFID 56 72
 FT DISULFID 71 125
 FT DISULFID 78 118
 FT DISULFID 87 111
 FT DISULFID 105 116
 FT METAL 55 55

FT METAL 57 57 Calcium (via carbonyl oxygen) (By similarity).
 FT METAL 76 76 Calcium (By similarity).
 SQ SEQUENCE 145 AA; 16002 MW; 38E36029AB5FA9 CRC64;
 Query Match 89.5%; Score 34; DB 1; Length 145;
 Best Local Similarity 71.4%; Pred. No. 50;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CXPXTC 7
 Db 105 CDPXTC 111

RESULT 10
 PRELIMINARY; PRT; 167 AA.
 ID Q7U7V9
 AC Q7U7V9
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical precursor.
 GN Ordered locus names=SYNW0871;
 OS Synecococcus sp. (strain WH8102).
 OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
 OX NCBI_TaxID=84588;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
 RA Paten B., Brahman B., Larimer F.W., Land M.L., Hauser L., Chait P., Lamer J.E., Regala W., Allen E.E., McCarron J., Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
 RL "The genome of a mobile marine Synecococcus".
 DR Nature 424:1037-1042 (2003).
 DR EMBL; BX569691; CAB07386.1; -
 KW Complete proteome; Hypothetical protein; Signal.
 FT SIGNAL 1 22
 FT SIGNAL 167 AA; 18419 MW; 0B3AFB830ECF971C CRC64;
 SQ SEQUENCE 167 AA; 18419 MW; 0B3AFB830ECF971C CRC64;

Query Match 89.5%; Score 34; DB 2; Length 167;
 Best Local Similarity 71.4%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CXPXTC 7
 Db 133 CYPXTC 139

RESULT 11
 PRELIMINARY; PRT; 312 AA.
 ID Q9SUJ3
 AC Q9SUJ3
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein P8B4.80 (Hypothetical protein A7432380).
 GN Name=P8B4.80; Synonym=AT4932380;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Arabidopsida; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Eukaryota; Viridiplantae; Streptophyta; eudicotyledons; core eudicots; rosids;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eudicots II; Brassicales; Brassicaceae; Arabidopsida.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP Bevan M., Terry N., Ardiles W., Buyssehaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villarejo R., Gielens J., Van Montagu M., Hohlefeld J., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
 RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RP EU Arabidopsis sequencing project;
 RL Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.

[3]
 RP SEQUENCE FROM N.A.
 RA Terry N., Argiles W., Buyschaert C., Daseville R., De Clerck R.,
 RA De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villarcel R.,
 RA Giesen J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.,
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 (4)
 RN SEQUENCE FROM N.A.
 RP EU Arabidopsis sequencing project;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
 DR EMBL: AL034567; CA22565.1; -.
 DR EMBL: AL161581; CAB79955.1; -.
 DR PIR: T05348; T05348.
 DR GO: GO:0004650; F:polysaccharonase activity; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR000743; Glyco_hydro_28.
 DR InterPro: IPR006626; Pbh1.
 DR InterPro: IPR01050; Pectin_lyase_like.
 DR Pfam: PF00295; Glyco_hydro_28; 2.
 DR SMART: SM00710; Pbh1; 3.
 DR Cell wall; Glycosidase; Hydrolase; Hypothetical protein.
 KW SEQUENCE 312 AA; 34095 MW; E2E70A2622F30BE0 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 312;
 Best Local Similarity 71.4%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXPXTGC 7
 DB 208 CVPRTGC 214

RESULT 12
 ID 06TVH9 PRELIMINARY; PRT; 465 AA.
 AC 06TVH9,
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Bovine Papular stomatitis virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Parapoxvirus.
 NCBI_TaxID=129727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BV-AR02;
 RX PubMed=14671098;
 RA Delhon G., Tulman E.R., Alfonso C.L., Lu Z., Piccone M.E., Kutish G.F.,
 RA de la Concha-Bermujillo A., Lemkuhl H.D., Piccone M.E., Kutish G.F.,
 RA Rock D.L.;
 RA "Genomes of the Parapoxviruses Orf Virus and Bovine Papular
 RA Stomatitis Virus."
 RT J. Virol. 78:168-177(2004).
 RL J. Virol. 78:168-177(2004).
 DR EMBL: AY386265; AAR98366.1; -.
 DR InterPro: IPR007027; Pox_F11.
 DR Pfam: PF04943; Pox_F11; 1.
 DR Hypothetical protein.
 KW SEQUENCE 465 AA; 51404 MW; BD735469CBED1B79 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 465;
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXPXTGC 7
 DB 26 CVPRTGC 32
 RESULT 13
 AAR98366 PRELIMINARY; PRT; 465 AA.
 ID AAR98366

AC AAR98366;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Bovine Papular stomatitis virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Parapoxvirus.
 NCBI_TaxID=129727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BV-AR02;
 RX PubMed=14671098;
 RA Delhon G., Tulman E.R., Alfonso C.L., Lu Z., Piccone M.E., Kutish G.F.,
 RA de la Concha-Bermujillo A., Lemkuhl H.D., Piccone M.E., Kutish G.F.,
 RA Rock D.L.;
 RA "Genomes of the Parapoxviruses Orf Virus and Bovine Papular
 RA Stomatitis Virus."
 RT J. Virol. 78:168-177(2004).
 RL J. Virol. 78:168-177(2004).
 DR EMBL: AY386265; AAR98366.1; -.
 DR Hypothetical protein.
 KW SEQUENCE 465 AA; 51404 MW; BD735469CBED1B79 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 465;
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXPXTGC 7
 DB 26 CVPRTGC 32

RESULT 14
 ID 08LJ36 PRELIMINARY; PRT; 574 AA.
 AC 08LJ36;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE P0413G02.18 protein.
 GN Name=P0413G02.18;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhacridae; Oryzae; Oryza.
 NCBI_TaxID=39477;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
 RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 RA Hishikawa S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
 RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwachi A., Kamiya K.,
 RA Karsawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
 RA Machida K., Maehara T., Mizuno H., Matsuhashi T., Mukai Y.,
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Tetsawa K., Teuji K.,
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshitara R., Yukawa K.,
 RA Zhong H., Iwama H., Ando T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
 RA Yano M., Jiang J., Gojobori T.;
 RT "The genome sequence and structure of rice chromosome 1."
 RL Nature 420:312-316(2002).
 DR EMBL: AP003344; BAC07361.1; -.
 DR HSSP: P20142; IAVF.
 DR Gramene; 08LJ36; -.
 DR GO: GO:0004194; F:pepsin A activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR001461; Peptidase A1.
 DR InterPro: IPR009007; Pept_Aspartic.
 DR Pfam: PF00026; Asp; 1.
 DR PRINTS; PR00792; PEPSIN.

8Q SEQUENCE 574 AA; 60980 MW; A2D654446084F35F CRC64;

Query Match 89.5%; Score 34; DB 2; Length 574;

Best Local Similarity 71.4%; Pred. No. 1.9e+02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXPXTGC 7

DB 119 CXPXTGC 125

Result 15

Q869K4 PRELIMINARY; PRT; 998 AA.

AC Q869K4; 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Similar to Mus musculus (Mouse). Tenascin X.

OS Dictyostelium discoideum (Slime mold).

OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.

OX NCBI_TaxID=44689;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=AX4;

RA Baumgart C.;

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC115598; AAC53206.1; -.

DR HSPF; P01132; 1EGF; Structural molecule activity; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR006209; EGF_2.

DR InterPro; IPR006210; EGF_1like.

DR InterPro; IPR002049; Laminin_EGF.

DR Pfam; PF00008; EGF; 7.

DR PRINTS; PR00011; EGF_LAMININ.

DR SMART; SM00181; EGF; 9.

DR PROSITE; PS00022; EGF_1; UNKNOWN_10.

DR PROSITE; PS01186; EGF_2; 7.

DR PROSITE; PS50026; EGF_3; 6.

SO SEQUENCE 998 AA; 106001 MW; F79BEF394D3E2369 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 998;

Best Local Similarity 71.4%; Pred. No. 3.1e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXPXTGC 7

DB 609 CXPXTGC 615

Search completed: January 12, 2005, 23:15:11

Job time : 88.55 sec

Nothing

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2005, 22:55:47 ; Search time 79.1 Seconds
(without alignment)
31.746 Million cell updates/sec

Title: US-09-932-322-8

Perfect score: 38

Sequence: 1 CKPXTGC 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_genseq238p04:*
2: geneseqp19808:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	92.1	79	4	AAU49413
2	35	92.1	79	6	ABM45932
3	35	92.1	180	7	ABO74428
4	34	89.5	7	3	AAV62764
5	34	89.5	7	3	AAV61489
6	34	89.5	7	3	AAV62007
7	34	89.5	7	3	AAV62224
8	34	89.5	7	5	ABJ00550
9	34	89.5	7	5	ABG33862
10	34	89.5	13	5	ABJ00545
11	34	89.5	13	5	ABG33861
12	34	89.5	53	4	AAU44932
13	34	89.5	53	6	ABM41451
14	34	89.5	113	6	ADA54961
15	34	89.5	138	3	AAV62037
16	34	89.5	250	7	ABO75329
17	34	89.5	312	5	ABB93198
18	34	89.5	540	7	ADP05702
19	34	89.5	3226	4	ABG28408
20	33	86.8	158	6	AAU40006
21	33	86.8	158	6	ABM46525
22	32	84.2	751	3	AAV63626
23	32	84.2	798	3	AAV63625
24	32	84.2	835	3	AAV63624
25	31	81.6	7	3	AAV63264

26	31	81.6	90	7	ABO81251	ABO81251 Pseudomon
27	31	81.6	114	5	ABP06368	ABP06368 Human ORF
28	31	81.6	148	7	ADJ71040	ADJ71040 Human hea
29	31	81.6	183	3	ADF58925	ADF58925 Human pol
30	31	81.6	193	4	AAO00015	AAO00015 Human pol
31	31	81.6	193	3	ADF60298	ADF60298 Human con
32	31	81.6	238	6	ABP99259	ABP99259 Orthosomy
33	31	81.6	239	6	ABP99348	ABP99348 Orthosomy
34	31	81.6	239	6	ABP76713	ABP76713 Streptomy
35	31	81.6	310	7	ABO74638	ABO74638 Pseudomon
36	31	81.6	444	7	ABO70819	ABO70819 Pseudomon
37	31	81.6	482	5	ABB93340	ABB93340 Herbicida
38	31	81.6	580	2	AAW32363	AAW32363 Mycobacte
39	31	81.6	580	2	AAW32431	AAW32431 Mycobacte
40	31	81.6	580	2	AAW64303	AAW64303 Mycobacte
41	31	81.6	580	2	AAW81666	AAW81666 M. tuberc
42	31	81.6	580	2	AAV38968	AAV38968 M. tuberc
43	31	81.6	580	2	AAV39105	AAV39105 M. tuberc
44	31	81.6	602	2	AAV04996	AAV04996 Mycobacte
45	31	81.6	638	2	AAV04992	AAV04992 Mycobacte

ALIGNMENTS

RESULT 1	AAU49413	AAU49413 standard; protein; 79 AA.
ID	AAU49413	
XX	AAU49413;	
DT	13-FEB-2002	(first entry)
DE	Propionibacterium acnes immunogenic protein #10309.	
XX		
KM	SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;	
KM	uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;	
KM	inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;	
KM	dermatological; osteopathic; neuroprotectant.	
XX		
OS	Propionibacterium acnes.	
XX		
PN	WO200181581-A2.	
PD		
XX	01-NOV-2001.	
XX		
PF	20-APR-2001; 2001WO-US012865.	
XX		
PR	21-APR-2000; 2000US-0199047P.	
PR	02-JUN-2000; 2000US-0208841P.	
PR	07-JUL-2000; 2000US-0216747P.	
XX		
PA	(CORI-) CORIXA CORP.	
XX		
PI	Skelky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;	
PI	L'maisonneuve J, Zhang Y, Jen S, Carter D;	
PT	N-PSDB; AAS59545.	
PT	Propionibacterium acnes polypeptides and nucleic acids useful for	
PT	vaccinating against and diagnosing infections, especially useful for	
PT	treating acne vulgaris.	
XX		
PS	Example 1, SEQ ID NO 10608; 10699p; English.	
XX		
CC	Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic	
CC	polypeptides. The proteins and their associated DNA sequences are used in	
CC	the treatment, prevention and diagnosis of medical conditions caused by	
CC	P. acnes. The disorders include SAPHO syndrome (synovitis, acne,	
CC	pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.	
CC	P. acnes is also involved in infections of bone, joints and the central	
CC	nervous system, however it is particularly involved in the inflammatory	

CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of *P. acnes* in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for *P. acnes* proteins. These antibodies can be used to
 CC downregulate expression and activity of *P. acnes* polypeptides and
 CC therefore treat *P. acnes* infections. The antibodies may also be used as
 CC diagnostic agents for determining *P. acnes* presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

CC Sequence 79 AA;

Query Match 92.1%; Score 35; DB 4; Length 79;
 Best Local Similarity 71.4%; Pred. No. 55;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXPXTGC 7
 Db 3 CSPGTGC 9

RESULT 2

ABM45932 ABM45932 standard; protein; 79 AA.

AC ABM45932;

DT 20-OCT-2003 (first entry)

DE Propionibacterium acnes predicted ORF-encoded polypeptide #10608.

XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;

KM immunostimulant; immune response; vaccine.

OS Propionibacterium acnes.

XX WO2003033515-A1.

XX 24-APR-2003.

XX 11-OCT-2002; 2002WO-US032727.

XX 15-OCT-2001; 2001US-00978825.

XX (CORI-) CORIXA CORP.

XX Mitcham JL, Skeiky YAM, Persing DH, Bhattacharya A, Maisonneuve JL,
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Valliave-Douglais J;

XX WPI; 2003-381789/36.

XX N-PSDB; ACF64474.

XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a *P. acnes* protein.

XX Example 1, SEQ ID NO 10608; 1481bp; English.

XX The invention relates to an isolated polynucleotide (ACF64435-ACF64473)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of *P. acnes* polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention, antibodies against polypeptides of the
 CC invention, fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a *P. acnes*
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising *P. acnes* polypeptides,

CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of *P. acnes* in a
 CC patient; and a method for inhibiting the development of *P. acnes* in a
 CC patient. The *P. acnes* polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a *P. acnes*
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridization. The vaccine composition is useful for the
 CC stimulation of an immune response against *P. acnes*, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the *P. acnes* polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

CC Sequence 79 AA;

Query Match 92.1%; Score 35; DB 6; Length 79;
 Best Local Similarity 71.4%; Pred. No. 55;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXPXTGC 7
 Db 3 CSPGTGC 9

RESULT 3

ABO74428 ABO74428 standard; protein; 180 AA.

AC ABO74428;

DT 29-JUL-2004 (first entry)

DE Pseudomonas aeruginosa polypeptide #6603.

XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX Pseudomonas aeruginosa.

XX US6551795-B1.

XX 22-APR-2003.

XX 18-FEB-1999; 99US-00252991.

XX 18-FEB-1998; 98US-0074788P.

XX 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nollig J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

XX N-PSDB; ABD07999.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.

XX Disclosure; SEQ ID NO 23174; 455bp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-*P. aeruginosa* drugs, as templates for recombinant

CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html

CC Sequence 180 AA;

Query Match 92.1%; Score 35; DB 7; Length 180;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC 1 CXPXTGC 7

DB 124 CRPATGC 130

RESULT 4

AA62764 ID AAY62764 standard; peptide; 7 AA.

XX AAY62764;

DT 02-MAR-2000 (first entry)

DE PB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:4047.

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
KW inhibition; cadherin extracellular domain; cell adhesion recognition; 12;
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease; cyclic.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

PT Disulfide-bond 1..7

FN W0957149-A2.

XX 11-NOV-1999.

PD 05-MAY-1999; 99WO-CA000363.

XX 05-MAY-1998; 98US-00073040.

PR 06-NOV-1998; 98US-00187859.

PR 20-JAN-1999; 99US-00234395.

PR 08-MAR-1999; 99US-00264516.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Gour BJ, Byers S;

XX WPI; 2000-038791/03.

XX New cadherin modulating agents, used for modulating nonclassical cadherin

PT arthritits, multiple sclerosis, diabetes or a neurological disease.

XX Claim 72; Page 193; 252pp; English.

XX The present invention describes cadherin modulating agents (MA)

CC comprising peptides which comprise a nonclassical cadherin cell adhesion

CC recognition (CAR) sequence. The MA can be used for modulating

CC nonclassical cadherin-mediated functions. They can be used for e.g.

CC inhibiting adhesion of nonclassical-cadherin expressing cells in a

CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC related macular degeneration, multiple sclerosis and diabetes.
CC The products can also be used for detection and diagnosis and in bioreactors.
CC AAY60592 to AAY64572 represent specifically claimed peptides, and
CC AAY64573 to AAY64643 and AAY64644 to AAY64645 represent sequences used in
CC the exemplification of the present invention

CC Sequence 7 AA;

Query Match 89.5%; Score 34; DB 3; Length 7;

Best Local Similarity 71.4%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC 1 CXPXTGC 7

DB 1 CDPXTGC 7

RESULT 5

AA61489 ID AAY61489 standard; peptide; 7 AA.

XX AAY61489;

DT 02-MAR-2000 (first entry)

DE Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1375.

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
KW inhibition; cadherin extracellular domain; cell adhesion recognition;
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease; cyclic.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

PT Disulfide-bond 1..7

FN W0957149-A2.

XX 11-NOV-1999.

PD 05-MAY-1999; 99WO-CA000363.

XX 05-MAY-1998; 98US-00073040.

PR 06-NOV-1998; 98US-00187859.

PR 20-JAN-1999; 99US-00234395.

PR 08-MAR-1999; 99US-00264516.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Gour BJ, Byers S;

XX WPI; 2000-038791/03.

XX New cadherin modulating agents, used for modulating nonclassical cadherin

PT arthritits, multiple sclerosis, diabetes or a neurological disease.

PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX
 PS Claim 36, Page 172, 252pp; English.

XX The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MA can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC -related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
 CC the exemplification of the present invention

XX Sequence 7 AA;

Query Match 89.5%; Score 34; DB 3; Length 7;
 Best Local Similarity 71.4%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXPXTGC 7
 DB 1 CXPXTGC 7

RESULT 6
 AAY62007
 ID AAY62007 standard; peptide; 7 AA.

XX AAY62007;

XX 02-MAR-2000 (first entry)

DE Cadherin-12 cell adhesion recognition cyclic peptide SEQ ID NO:11799.

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.

XX Synthetic.
 OS Homo sapiens.

XX Key Location/Qualifiers

XX Disulfide-bond 1. 7
 XX MO9957149-A2.

XX 11-NOV-1999.

XX 05-MAY-1999; 99WO-CA000363.

XX 05-MAY-1998; 98US-00073040.

XX 06-NOV-1998; 98US-00187859.

PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Gour BJ, Byers S;

XX WPI, 2000-038791/03.

XX New cadherin modulating agents, used for modulating nonclassical cadherin
 PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX
 PS Claim 48; Page 180; 252pp; English.

XX The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MA can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC -related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
 CC the exemplification of the present invention

XX Sequence 7 AA;

Query Match 89.5%; Score 34; DB 3; Length 7;
 Best Local Similarity 71.4%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXPXTGC 7
 DB 1 CXPXTGC 7

RESULT 7
 AAY62224
 ID AAY62224 standard; peptide; 7 AA.

XX AAY62224;

XX 02-MAR-2000 (first entry)

DE Cadherin-14 cell adhesion recognition cyclic peptide SEQ ID NO:3971.

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.

XX Synthetic.
 OS Homo sapiens.

XX Key Location/Qualifiers

FT Disulfide-bond 1. 7
 XX
 XX WO957149-A2.
 XX
 PD 11-NOV-1999.
 XX
 XX 05-MAY-1999; 99WO-CA000363.
 XX
 XX 05-MAY-1998; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 XX Blaschuk OM, Gour BJ, Byers S;
 PI WPI, 2000-038791/03.
 DR
 XX
 PT New cadherin modulating agents, used for modulating nonclassical cadherin
 PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX
 XX Claim 54; Page 184; 252pp; English.
 PS
 XX The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC -related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AA23183 to AA23186 represent sequences used in
 CC the exemplification of the present invention
 CC
 XX
 SQ Sequence 7 AA;
 Query Match 89.5%; Score 34; DB 3; Length 7;
 Best Local Similarity 71.4%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CXPXTGC 7
 DB 1 CDPXTGC 7
 ID ABO0550 standard; peptide; 7 AA.
 AC ABO0550;
 XX
 DT 05-SBP-2002 (first entry)
 XX
 DE B lymphocyte stimulator protein binding peptide #1.
 XX
 KW B lymphocyte stimulator protein binding protein; Blys; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 XX

KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritis;
 KW neuroprotective; cytostatic; immunostimulant; antitumor; anti-HIV;
 KW antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;
 KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.
 XX
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 2
 FT Misc-difference /label= Phe, Trp, Tyr
 FT Misc-difference 4
 FT Misc-difference /label= Pro, Tyr
 FT
 XX
 XX WO200216411-A2.
 XX
 XX PD 28-FEB-2002.
 XX
 XX
 PR 17-AUG-2001; 2001WO-US025850.
 XX
 PR 18-AUG-2000; 2000US-0226700P.
 XX
 XX (HDMA-) HUMAN GENOME SCI INC.
 PA
 XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
 PI WPI, 2002-499775/53.
 DR
 XX
 XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
 PT administering B lymphocyte stimulator binding polypeptide.
 PT
 PS Claim 69; Page 233; 387pp; English.
 XX
 XX The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of Blys binding polypeptide.
 CC The Blys binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of haematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein binding peptide
 CC
 XX
 SQ Sequence 7 AA;
 Query Match 89.5%; Score 34; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXPXTGC 7
 DB 1 CXPXTGC 7
 ID ABG33862 standard; peptide; 7 AA.
 AC ABG33862;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE B lymphocyte stimulator (Blys) binding peptide #436.
 XX
 KW B lymphocyte stimulator protein; B lymphocyte stimulator binding peptide;
 KW Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
 KW synovial fluid; saliva; mucus.
 XX

OS Synthetic.
 XX MO200216412-A2.
 XX
 XX 28-FEB-2002.
 XX
 XX 17-AUG-2001; 2001MO-US025891.
 XX
 XX 18-AUG-2000; 2000US-0226489P.
 XX
 XX (DYAX-) DYAX CORP.
 PA
 PI Beltzer JP, Potter MD, Fleming TJ, Ladner RC;
 XX WPI; 2002-351647/38.
 XX
 XX New B-lymphocyte stimulator binding polypeptide useful in detecting or
 PT isolating Blys or Blys-like polypeptide comprises a specified amino acid
 PT sequence.
 XX
 XX Disclosure; Page 132; 269pp; English.
 PS
 XX The invention relates to a B lymphocyte stimulator (Blys) binding
 CC polypeptide. Blys binding peptides bind Blys or Blys-like proteins
 CC reversibly or irreversibly. The binding peptides are used in detection,
 CC isolation and/or purification of Blys in a solution such as water or a
 CC buffer solution, as well as any fluid and/or cell obtained from an
 CC individual biological fluid, body tissue, body cell, cell line, tissue
 CC culture or other source containing Blys or Blys-like polypeptides. The
 CC biological fluids include sera, plasma, lymph, blood, blood fraction,
 CC urine, synovial fluid, spinal fluid, saliva and mucous. Sequences
 CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
 CC ABG33852-33862 represent Blys binding peptides of the invention
 CC
 SQ Sequence 7 AA;
 Query Match 89.5%; Score 34; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXPXTGC 7
 DB 1 CXPXTGC 7
 RESULT 10
 ABJ00545
 ID ABJ00545 standard; peptide; 13 AA.
 AC ABJ00545;
 XX
 XX 05-SEP-2002 (first entry)
 DT
 XX
 XX B lymphocyte stimulator protein binding protein consensus peptide #1.
 XX
 XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinemia; blood clotting;
 KW leukaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
 KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
 KW antiaesthetic; anti-allergic; thyromimetic; antianemic; haemostatic;
 KW dermatological; anti-inflammatory; cardiac; ophthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.
 XX
 XX Undenitrified.
 OS
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 1 /label= Ala, Asn, Lys, Ser
 FT Misc-difference 2 /label= Ala, Glu, Met, Ser, Val
 FT Misc-difference 3

FT /label= Ala, Asn, Lys, Pro
 FT Misc-difference 5 /label= Phe, Trp, Tyr
 FT
 FT Misc-difference 7 /label= Pro, Tyr
 FT
 FT Misc-difference 11 /label= Ala, Glu, His, Phe, Val
 FT
 FT Misc-difference 12 /label= Asn, Glu, Gly, His, Ser, Val
 FT
 FT Misc-difference 13 /label= Ala, Asn, Gly, Ile, Pro, Ser
 FT
 XX
 XX MO200216411-A2.
 XX
 XX 28-FEB-2002.
 XX
 XX 17-AUG-2001; 2001MO-US025850.
 XX
 XX 18-AUG-2000; 2000US-0226700P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Beltzer JP, Potter DM, Fleming TJ, Rosen CA;
 XX WPI; 2002-499775/53.
 XX
 XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
 PT administering B lymphocyte stimulator binding polypeptide.
 PT
 XX Claim 69; Page 230; 387pp; English.
 PS
 XX The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of Blys binding polypeptide.
 CC The Blys binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of haematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinemia, blood clotting disorders, leukaemia, and
 CC neurodegenerative diseases. The present sequence is a conserved region of
 CC a B lymphocyte stimulator protein binding peptide
 CC
 SQ Sequence 13 AA;
 Query Match 89.5%; Score 34; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXPXTGC 7
 DB 4 CXPXTGC 10
 RESULT 11
 ABG33861
 ID ABG33861 standard; peptide; 13 AA.
 AC ABG33861;
 XX
 XX 15-JUL-2002 (first entry)
 DT
 XX
 XX B lymphocyte stimulator (Blys) binding peptide #43.
 XX
 XX B lymphocyte stimulator protein; B lymphocyte stimulator binding peptide;
 KW Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
 KW synovial fluid; saliva; mucus.
 XX
 XX Synthetic.
 OS
 XX
 XX MO200216412-A2.

```
XX 28-FEB-2002.
PD 17-AUG-2001; 2001WO-US025891.
XX 18-AUG-2000; 2000US-0226489P.
XX (DYAX-) DYAX CORP.
PA Belzer JP, Potter MD, Fleming TJ, Ladner RC,
XX WPI, 2002-351647/38.
XX New B-lymphocyte stimulator binding polypeptide useful in detecting or
PT isolating Blys or Blys-like polypeptide comprises a specified amino acid
PT sequence.
XX Discloure; Page 121; 269pp; English.
XX The invention relates to a B lymphocyte stimulator (Blys) binding
CC polypeptide. Blys binding peptides bind Blys or Blys-like proteins
CC reversibly or irreversibly. The binding peptides are used in detection,
CC isolation and/or purification of Blys in a solution such as water or a
CC buffer solution, as well as any fluid and/or cell obtained from an
CC individual biological fluid, body tissue, body cell, cell line, tissue
CC culture or other source containing Blys or Blys-like polypeptides. The
CC biological fluids include sera, plasma, lymph, blood, blood fraction,
CC urine, synovial fluid, spinal fluid, saliva and mucous. Sequences
CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
CC ABG33852-33862 represent Blys binding peptides of the invention
XX.
SQ Sequence 13 AA;
Query Match 89.5%; Score 34; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXPXTGC 7
Db 4 CXPXTGC 10
RESULT 12
AAU44932
ID AAU44932 standard; protein; 53 AA.
XX AAU44932;
AC
XX 27-FEB-2002 (first entry)
DT
XX Propionibacterium acnes immunogenic protein #5828.
DE
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
XX Propionibacterium acnes.
OS
XX WO200181581-A2.
XX
XX 01-NOV-2001.
PD
XX 20-APR-2001; 2001WO-US012865.
XX
XX 21-APR-2000; 2000US-0199047P.
XX 02-JUN-2000; 2000US-0208841P.
XX 07-JUL-2000; 2000US-0216747P.
XX
XX (CORI-) CORIXA CORP.
PA
XX Skelky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A,
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
```

```
XX WPI; 2001-616774/71.
DR N-PSDB; AAS59524.
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
XX Example 1; SEQ ID NO 6127; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX.
SQ Sequence 53 AA;
Query Match 89.5%; Score 34; DB 4; Length 53;
Best Local Similarity 71.4%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CXPXTGC 7
Db 33 CRPXTGC 39
RESULT 13
ABM41451
ID ABM41451 standard; protein; 53 AA.
XX ABM41451;
AC
XX 20-OCT-2003 (first entry)
DT
XX Propionibacterium acnes predicted ORF-encoded polypeptide #6127.
DE
XX Acne vulgaris; antiheborrheic; dermatological; antibacterial;
KW immunostimulant; immune response; vaccine.
XX
XX Propionibacterium acnes.
OS
XX WO2003033515-A1.
XX
XX 24-APR-2003.
PD
XX 11-OCT-2002; 2002WO-US032727.
XX
XX 15-OCT-2001; 2001US-00978825.
XX
XX (CORI-) CORIXA CORP.
PA
XX Mitcham JL, Skelky YAW, Persing DH, Bhatia A, Maisonneuve J;
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
PI Barch B, Vallieye-Douglass J;
XX WPI; 2003-381789/36.
DR N-PSDB; ACP64453.
```

XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PI or for stimulating an immune response specific for a P. acnes protein.
XX

XX Example 1, SEQ ID NO 6127, 1481bp, English.

XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
XX encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention; antibodies against polypeptides of the
CC invention; fusion proteins comprising a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising T cells prepared
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX

XX Sequence 53 AA;

Query Match 89.5%; Score 34; DB 6; Length 53;
Best Local Similarity 71.4%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXPXTGC 7
DB 33 CRPRTGC 39

RESULT 14

ADA54961 standard; protein, 113 AA.

XX ADA54961;

XX 20-NOV-2003 (first entry)

XX Human protein, SEQ ID 2529.

XX Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nocotropic;
KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW inflammatory disease; osteoporosis; neurological disease.
XX

XX Homo sapiens.

XX BPI293569-A2.

XX 19-MAR-2003.

XX 21-MAR-2002; 2002EP-00005686.

XX 14-SEP-2001; 2001JP-00328381.

XX 24-JAN-2002; 2002US-0350435P.

XX (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,
PI Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuho Y,
XX
DR WPI, 2003-395539/38.
DR N-PSDB; ADA53322.

XX New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PI which the gene is involved, or as target molecules for gene therapy.

XX Claim 14; SEQ ID NO 2529, 205bp, English.

XX The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
CC inflammatory diseases, osteoporosis or neurological disease.

XX Sequence 113 AA;

Query Match 89.5%; Score 34; DB 6; Length 113;
Best Local Similarity 71.4%; Pred. No. 1,1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXPXTGC 7
DB 103 CXPXTGC 109

RESULT 15

ABA42027 standard; protein, 138 AA.

XX ABA42027;

XX 08-FEB-2001 (first entry)

XX Human ORFX ORF1791 polypeptide sequence SEQ ID NO:3582.

XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnery; antiparasitic; antiparkinsonian; nocotropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antihemetic; antihypoid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; achma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive.

XX Homo sapiens.

XX WO200058473-A2.

XX 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US008621.

XX 31-MAR-1999; 99US-0127607P.

XX 02-APR-1999; 99US-0127636P.

XX 05-APR-1999; 99US-0127728P.

XX 30-MAR-2000; 2000US-00540763.

XX (CURA-) CURAGEN CORP.
PA Shinketsu RA, Leach M;
XX PI

DR WPI; 2000-602362/57.
 DR N-PSDB; AAC76236.
 PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease.

Claim 11, Page 2743; 5507pp; English.

AACT4446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 which represent the human ORF open reading frames 1 to 3161. The ORF
 sequences have activities such as: cytostatic; hepatotropic; vulnery;
 antiproliferative; antiparkinsonian; nootropic; neuroprotective; osteopathic;
 anticonvulsant; antidiabetic; immunosuppressant; immunostimulant;
 cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 dermatological; immunosuppressive; antineoplastic; antibacterial;
 antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
 sequences can be used for determining the presence of or predisposition
 to, or preventing or treating pathological conditions associated with an
 ORF-associated disorder. The nucleic acids can be used to express ORF
 proteins in gene therapy vectors. The proteins and nucleic acids may be
 used to treat cancers, proliferative disorders, neurodegenerative
 disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
 storage, systemic lupus erythematosus, severe combined immunodeficiency
 (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
 disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
 cartilage damage, nocturnal haemoglobinuria, antineoplastic disease; to
 enhance coagulation; to inhibit thrombosis; and as a contraceptive

Sequence 138 AA;

Query Match 89.5%; Score 34; DB 3; Length 138;
 Best Local Similarity 71.4%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXPXTGC 7
 DB 15 CXPXTGC 21

Search completed: January 12, 2005, 23:10:52
 Job time : 79.1 secs